

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 11:09:47 ; Search time 97 Seconds
(without alignments)
5337.827 Million cell updates/sec

Title: US-10-079-137B-343

Perfect score: 933
Sequence: 1 atgggtggtgaggtgtatc.....tggtttctagcatcatcatg 933

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
2	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
3	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
4	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
5	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
6	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
7	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
8	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
9	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
10	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
11	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
12	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
13	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
14	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
15	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
16	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
17	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
18	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
19	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
20	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
21	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
22	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
23	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
24	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
25	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
26	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
27	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App

ALIGNMENTS

RESULT 1

US-09-439-313-531

; Sequence 531, Application US/09439313

; Patent No. 6329505

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan Louise

; APPLICANT: Jiang Yuqui

; APPLICANT: Reed, Steven G.

; APPLICANT: Kalos, Michael

; APPLICANT: Fanger, Gary

; APPLICANT: Retter, Mark

; APPLICANT: Solk, John

; APPLICANT: Day, Craig

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

; FILE REFERENCE: 210121.427C9

; CURRENT APPLICATION NUMBER: US/09/439,313

; CURRENT FILING DATE: 1999-11-12

; NUMBER OF SEQ ID NOS: 575

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 531

; LENGTH: 879

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-439-313-531

Query Match 89.2%; Score 831.8; DB 4; Length 879;

Best Local Similarity 99.8%; Pred. No. 4.4e-238;

Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	99	CAGGGGGAGCGGCAAGAGCAACGTTGGGGCACTTCTGGAGACCAACGACTCTCTGTGAA	158
DB	42	CAGGGGGAGCGGCAAGAGCAACGTTGGGGCACTTCTGGAGACCAACGACTCTCTGTGAA	101
QY	159	GACGCTTGGGAGCAAGAGTGCAGTGTGTGTGCACTGCTTCCCTCTGTCAGGGGAG	218
DB	102	GACGCTTGGGAGCAAGAGTGCAGTGTGTGTGCACTGCTTCCCTCTGTCAGGGGAG	161
QY	219	CGGCAAGAGCAACGTTGGGGCACTTGGGGAGATACGATGACAGCGCTTCATGGATCCAG	278
DB	162	CGGCAAGAGCAACGTTGGGGCACTTGGGGAGATACGATGACAGCGCTTCATGGATCCAG	221
QY	279	GTACCACCTCCATGAGAGATCTGGACAAGTCCACAGAGTGCCTGTGGGTAAAGT	338
DB	222	GTACCACCTCCATGAGAGATCTGGACAAGTCCACAGAGTGCCTGTGGGTAAAGT	281
QY	339	CCCCAGAAAGGATCTCATGCTCAGGGACACTGATGTGAACAAGAGGCAACGA	398

Db 282 CCCAGGAGGATCTCATCTGTCATGCTCAGGACACGGATGTGAACAAGGAGGACAAGCA 341
Qy 399 AAGAGGAGCTGCTTCACTCTGCGCTCTGCGAATGGGAATTCAGAAAGTAAACTGGT 458
Db 342 AAGAGGAGCTGCTTCACTCTGCGCTCTGCGAATGGGAATTCAGAAAGTAAACTGGT 401
Qy 459 GCTGGACAGACGATGCAACTTAATGTCCTTGACAAACAAAGAGGACAGCTCTGACAAA 518
Db 402 GCTGGACAGACGATGCAACTTAATGTCCTTGACAAACAAAGAGGACAGCTCTGACAAA 461
Qy 519 GCGCGTACAAATCCAGGAGATGAATGTGGTGAATGTTGCTGGAAACATGGCACTGATCC 578
Db 462 GCGCGTACAAATCCAGGAGATGAATGTGGTGAATGTTGCTGGAAACATGGCACTGATCC 521
Qy 579 AATATATCCAGATGAGTATGGAATACCACTCTACACTATGCTCTACAAATGAAGATAA 638
Db 522 AATATATCCAGATGAGTATGGAATACCACTCTACACTATGCTCTACAAATGAAGATAA 581
Qy 639 ATTAATGGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 698
Db 582 ATTAATGGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 641
Qy 699 CCTCACACCACTGCTACTGTTATATGATGATGACGACAAACAGCAAGTGGTGAATTTTAA 758
Db 642 CCTCACACCACTGCTACTGTTATATGATGATGACGACAAACAGCAAGTGGTGAATTTTAA 701
Qy 759 CAAGAAAAAGCGAATTTAAATCGCTGGATAGATATGGAAGCACTGCTCTCATCTGTC 818
Db 702 CAAGAAAAAGCGAATTTAAATCGCTGGATAGATATGGAAGCACTGCTCTCATCTGTC 761
Qy 819 TGATGTTGGATCAGCAAGTATAGTACGCTCTTATGATGATGACGACAAACAGCAAGTGGTGAATTTTAA 878
Db 762 TGATGTTGGATCAGCAAGTATAGTACGCTCTTATGATGATGACGACAAACAGCAAGTGGTGAATTTTAA 821
Qy 879 TTCTCAAGATCTGGAAGAGCGCCAGAGATGATGCTGTTTCTAGTCATCATCATG 933
Db 822 TTCTCAAGATCTGGAAGAGCGCCAGAGATGATGCTGTTTCTAGTCATCATCATG 876

RESULT 2

US-09-636-215-531
; Sequence 531, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Panger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Rasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 531
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-636-215-531
Query Match 89.2%; Score 831.8; DB 4; Length 879;
Best Local Similarity 99.8%; Pred. No. 4.4e-238;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 99 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCAACACGACTCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCAACACGACTCTCTGTGAA 101
Qy 159 GACCTTTGGGAGCAAGAGGTCGAAGTGGTGGCACTTCCCTGCTTCCCTGCTGCGAGGGGAG 218
Db 102 GACCTTTGGGAGCAAGAGGTCGAAGTGGTGGCACTTCCCTGCTTCCCTGCTGCGAGGGGAG 161
Qy 219 CGGCAAGAGCAACGTGGGCGCTTGGGGAGACTAGATGACAGCGCTTCATGATCCAG 278
Db 162 CGGCAAGAGCAACGTGGTGGTGGGAGACTAGATGACAGCGCTTCATGATCCAG 221
Qy 279 GTACACGTCCTGAGAGATCTGGAAGATCTGGAAGATCTGGAAGATCTGGAAGATCTGGAAGAT 338
Db 222 GTACACGTCCTGAGAGATCTGGAAGATCTGGAAGATCTGGAAGATCTGGAAGATCTGGAAGAT 281
Qy 339 CCCAGAAAGGATCTCATCTGCTCAGGGACACTGATGTGAACAAGAGGGGCAAGCA 398
Db 282 CCCAGAAAGGATCTCATCTGCTCAGGGACACTGATGTGAACAAGAGGGGCAAGCA 341
Qy 399 AAGAGGAGCTCTTACATCTGGCTCTGCCAATGGGAATTCAGAAAGTAAACTGGT 458
Db 342 AAGAGGAGCTCTTACATCTGGCTCTGCCAATGGGAATTCAGAAAGTAAACTGGT 401
Qy 459 GCTGGACAGACGATGTCAACTTAATGTCCTTGACAAACAAAGAGGAGGACAGCTCTGACAAA 518
Db 402 GCTGGACAGACGATGTCAACTTAATGTCCTTGACAAACAAAGAGGAGGACAGCTCTGACAAA 461
Qy 519 GCGCGTACAAATCCAGGAGATGAATGTGGTGAATGTTGCTGGAAACATGGCACTGATCC 578
Db 462 GCGCGTACAAATCCAGGAGATGAATGTGGTGAATGTTGCTGGAAACATGGCACTGATCC 521
Qy 579 AATATATCCAGATGAGTATGGAATACCACTCTACACTATGCTCTACAAATGAAGATAA 638
Db 522 AATATATCCAGATGAGTATGGAATACCACTCTACACTATGCTCTACAAATGAAGATAA 581
Qy 639 ATTAATGGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 698
Db 582 ATTAATGGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 641
Qy 699 CCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAA 758
Db 642 CCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAA 701
Qy 759 CAAGAAAAAGCGAATTTAAATGGCTGGATAGATATGGAAGCACTGCTCTCATCTGTC 818
Db 702 CAAGAAAAAGCGAATTTAAATGGCTGGATAGATATGGAAGCACTGCTCTCATCTGTC 761
Qy 819 TGATGTTGGATCAGCAAGTATAGTACGCTCTTATGATGATGACGACAAACAGCAAGTGGTGAATTTTAA 878
Db 762 TGATGTTGGATCAGCAAGTATAGTACGCTCTTATGATGATGACGACAAACAGCAAGTGGTGAATTTTAA 821
Qy 879 TTCTCAAGATCTGGAAGAGCGCCAGAGATGATGCTGTTTCTAGTCATCATCATG 933
Db 822 TTCTCAAGATCTGGAAGAGCGCCAGAGATGATGCTGTTTCTAGTCATCATCATG 876

RESULT 3

US-09-685-166A-531
; Sequence 531, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi

QY 579 AAATATTCAGATGAGTATGGAATACCACTCTACATGCTGTCTACAATGAAGATAA 638
 DB 522 AAATATTCAGATGAGTATGGAATACCACTCTACATGCTGTCTACAATGAAGATAA 581
 QY 639 AATATTCAGATGAGTATGGAATACCACTCTACATGCTGTCTACAATGAAGATAA 698
 DB 582 AATATTCAGATGAGTATGGAATACCACTCTACATGCTGTCTACAATGAAGATAA 641
 QY 699 CTTCAACCACTGCTACTTTGGTATACATGAGCAAAACAGCAAGTGGTGAATTTTAAAT 758
 DB 642 CTTCAACCACTGCTACTTTGGTATACATGAGCAAAACAGCAAGTGGTGAATTTTAAAT 701
 QY 759 CAAGAAAAAGCGAATTTAAATGCGTGTGATAGATGGAAGACTGCTCTACATCTTGC 818
 DB 702 CAAGAAAAAGCGAATTTAAATGCGTGTGATAGATGGAAGACTGCTCTACATCTTGC 761
 QY 819 TGTATGTTGGATCAGCAAGTATAGTCAAGCCCTCTACTTGAAGCAAAATGTTGATGATC 878
 DB 762 TGTATGTTGGATCAGCAAGTATAGTCAAGCCCTCTACTTGAAGCAAAATGTTGATGATC 821
 QY 879 TTCTCAAGATCTGGAAGACGGCAGAGATGATGCTGTTCTAGTCATCATCATG 933
 DB 822 TTCTCAAGATCTGGAAGACGGCAGAGATGATGCTGTTCTAGTCATCATCATG 876

RESULT 5
 US-09-439-313-530
 ; Sequence 530, Application US/09439313
 ; Patent No. 6329505
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan Louise
 ; APPLICANT: Jiang Yuqui
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Kalos, Michael
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Retter, Mark
 ; APPLICANT: Solk, John
 ; APPLICANT: Day, Craig
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 ; FILE REFERENCE: 210121.427C9
 ; CURRENT APPLICATION NUMBER: US/09/439,313
 ; CURRENT FILING DATE: 1999-11-12
 ; NUMBER OF SEQ ID NOS: 575
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 530
 ; LENGTH: 1852
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-439-313-530

Query Match 89.2%; Score 831.8; DB 4; Length 1852;
 Best Local Similarity 99.8%; Pred. No. 6.7e-238;
 Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 99 CAGGGGAGCGGCAAGCAACGTTGGGCACTTTGGGAGACCAAGCACTCTCTGTGAA 158
 DB 771 CAGGGGAGCGGCAAGCAACGTTGGGCACTTTGGGAGACCAAGCACTCTCTGTGAA 830
 QY 159 GACGCTTTGGGAGCAAGAGTGCAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 218
 DB 831 GACGCTTTGGGAGCAAGAGTGCAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 890
 QY 219 CGGCAAGCAACGTTGGGCGCTTTGGGAGACTACGATGACAGGCGCTTTCATGATCCAG 278
 DB 891 CGGCAAGCAACGTTGGTGGTGGGAGACTAGATGACAGGCGCTTTCATGATCCAG 950
 QY 279 GTACACAGTCCATGGAGAGATTCGACAGCTCCACAGAGCTGCTGTTGGGTTAAAGT 338
 DB 951 GTACACAGTCCATGGAGAGATTCGACAGCTCCACAGAGCTGCTGTTGGGTTAAAGT 1010

QY 339 CCCAGAAAGGATCTCATGCTCATGCTCAGGAGCACTGATGTGAAACAAGAGGCAAGCA 398
 DB 1011 CCCAGAAAGGATCTCATGCTCATGCTCAGGAGCACTGATGTGAAACAAGAGGCAAGCA 1070
 QY 399 AAAGAGACTGCTCTACATCTGCGCTCTGCCAATGGGAATTCAGAACTAGTAACCTCGT 458
 DB 1071 AAAGAGACTGCTCTACATCTGCGCTCTGCCAATGGGAATTCAGAACTAGTAACCTCGT 1130
 QY 459 GCTGGACAGACGATGTCAACTTAAATGCTTTGACCAACAAAGAGGACAGCTCTGACAAA 518
 DB 1131 GCTGGACAGACGATGTCAACTTAAATGCTTTGACCAACAAAGAGGACAGCTCTGACAAA 1190
 QY 519 GCGCGTACATGCGCAGGAAGATGAATGTGCGTTAAATGCTTGGTGGTGGTGGTGGTGGTGG 578
 DB 1191 GCGCGTACATGCGCAGGAAGATGAATGTGCGTTAAATGCTTGGTGGTGGTGGTGGTGGTGG 1250
 QY 579 AAATATTCAGATGAGTATGGAATACCACTCTACATGCTGTCTACATGCTGTCTACATGAGATAA 638
 DB 1251 AAATATTCAGATGAGTATGGAATACCACTCTACATGCTGTCTACATGAGATAA 1310
 QY 639 AATATTCAGATGAGTATGGAATACCACTCTACATGCTGTCTACATGAGATAA 698
 DB 1311 AATATTCAGATGAGTATGGAATACCACTCTACATGCTGTCTACATGAGATAA 1370
 QY 699 CCTCACACCACTGCTACTTTGCTATACATGAGCAAAACAGCAAGTGGTGAATTTTAAAT 758
 DB 1371 CCTCACACCACTGCTACTTTGCTATACATGAGCAAAACAGCAAGTGGTGAATTTTAAAT 1430
 QY 759 CAAGAAAAAGCGAATTTAAATGCGTGTGATAGATGGAAGAACTGCTCTACATCTTGC 818
 DB 1431 CAAGAAAAAGCGAATTTAAATGCGTGTGATAGATGGAAGAACTGCTCTACATCTTGC 1490
 QY 819 TGTATGTTGGATCAGCAAGTATAGTCAAGCCCTCTACTTTGAGCAAAATGTTGATGATC 878
 DB 1491 TGTATGTTGGATCAGCAAGTATAGTCAAGCCCTCTACTTTGAGCAAAATGTTGATGATC 1550
 QY 879 TTCTCAAGATCTGGAAGACGGCAGAGATGATGCTGTTCTAGTCATCATCATG 933
 DB 1551 TTCTCAAGATCTGGAAGACGGCAGAGATGATGCTGTTCTAGTCATCATCATG 1605

RESULT 6
 US-09-636-215-530
 ; Sequence 530, Application US/09636215
 ; Patent No. 6620922
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqui
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Solk, John H.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedwick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Vasil A.W.
 ; APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.42717C17
 ; CURRENT APPLICATION NUMBER: US/09/636,215
 ; CURRENT FILING DATE: 2000-08-10
 ; NUMBER OF SEQ ID NOS: 852
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 530
 ; LENGTH: 1852

[illegible]

RESULT 7
US-09-685-166A-530
; Sequence 530, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.

```

; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 530
; LENGTH: 1852
; TYPE: DNA
; ORGANISM: Homo sapiens
; IS-09-685-166A-530

```

Query Match	89.2%;	Score 831.8;	DB 4;	Length 1852;
Best Local Similarity	99.8%;	Pred. No. 6,7e-238;		
Matches 833;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	99	CAGGGGAGCGCAAGAGCAACGCTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA	158	
DB	771	CAGGGGAGCGCAAGAGCAACGCTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA	830	
QY	159	GACGCTTGGGACCAAGAGTGCAAGTGTGCTGCCACTCTTCCCTGCTGCAGGGGGAG	218	
DB	831	GACGCTTGGGACCAAGAGTGCAAGTGTGCTGCCACTCTTCCCTGCTGCAGGGGGAG	890	
QY	219	CGCGAAGAGCAACGCTGGGCGCTTGGGGAGACTACGATGACAGCGCTTTCATGGATCCCAG	278	
DB	891	CGCGAAGAGCAACGCTGGTTCGCTTGGGAGACTACGATGACAGCGCTTTCATGGATCCCAG	950	
QY	279	GTACCACTGTCATGAGAGAGATCTGGACAACTCCACAGAGTGCTGCTGGGGTAAAGT	338	
DB	951	GTACCACTGTCATGAGAGAGATCTGGACAACTCCACAGAGTGCTGCTGGGGTAAAGT	1010	
QY	339	CCCCAGAAGGATCTCATCGTCAATGCTCAGGGACACTGATGTGAAACAAGAGGGACAAAGCA	398	
DB	1011	CCCCAGAAGGATCTCATCGTCAATGCTCAGGGACACTGATGTGAAACAAGAGGGACAAAGCA	1070	
QY	399	AAAGAGGACTGCTTACATCTCTGGCTCTGCCAATGGGAATTCAGAAGTAGTAAACTCGT	458	
DB	1071	AAAGAGGACTGCTTACATCTCTGGCTCTGCCAATGGGAATTCAGAAGTAGTAAACTCGT	1130	
QY	459	GCTGGACAGACAGATGTCAACTTAATGTCTCTTGACAAACAAAAAGAGACAGCTCTGACAAA	518	
DB	1131	GCTGGACAGACAGATGTCAACTTAATGTCTCTTGACAAACAAAAAGAGACAGCTCTGACAAA	1190	
QY	519	GAGCGTGACATGCCAGGAAGATGAATGCGTTAATGTTGCTGGAACTGGCACTGATCC	578	
DB	1191	GAGCGTGACATGCCAGGAAGATGAATGCGTTAATGTTGCTGGAACTGGCACTGATCC	1250	
QY	579	AAATATCCAGATGAGTATGGAATACCACTTCACACTATGCTGTCTACAATGAAGATAA	638	
DB	1251	AAATATCCAGATGAGTATGGAATACCACTTCACACTATGCTGTCTACAATGAAGATAA	1310	
QY	639	ATTAATGGCCAAAGCACTGCTTTATACGGTGCTGATATCGAATCAAAAACCAAGCATGG	698	
DB	1311	ATTAATGGCCAAAGCACTGCTTTATACGGTGCTGATATCGAATCAAAAACCAAGCATGG	1370	
QY	699	CCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTTTAAT	758	

Db 1371 CCTCACCACTGCTACTTGGTATACATGAGCAAAACACAGCAAGTGGTGAATTTTAAAT 1430
QY 759 CAGAAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATATTGC 818
Db 1431 CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATATTGC 1490
QY 819 TGTATGTTGGATCAGCAAGTATAGTCAGCCCTCTACTTTGACAAATGTTGATGATC 878
Db 1491 TGTATGTTGGATCAGCAAGTATAGTCAGCCCTCTACTTTGACAAATGTTGATGATC 1550
QY 879 TTCTCAAGATCTGGAAGAGCGGCGAGAGATGCTGTTTCTAGTCATCATG 933
Db 1551 TTCTCAAGATCTGGAAGAGCGGCGAGAGATGCTGTTTCTAGTCATCATG 1605

RESULT 8

US-09-429-755-313
; Sequence 313, Application US/09429755A
; Patent No. 6656480
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 1852
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-429-755-313

Query Match 89.2%; Score 831.8; DB 4; Length 1852;
Best Local Similarity 99.8%; Pred. No. 6.7e-238;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTTCTGGAGCCCAAGCACTCTCTGTGAA 158
Db 771 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTTCTGGAGCCCAAGCACTCTCTGTGAA 830
QY 159 GACGCTTGGAGCAAGAGTGGTGGTCTGCTGCTTCCCTGCTGCGAGGGGAG 218
Db 831 GACGCTTGGAGCAAGAGTGGTGGTCTGCTGCTTCCCTGCTGCGAGGGGAG 890
QY 219 CGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGATGACAGCGCTTCAAGATCCGAG 278
Db 891 CGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGATGACAGCGCTTCAAGATCCGAG 950
QY 279 GTACCAGCTCCATGGAAGATCTGGCAAGCTCCACAGAGTCCCTGGTGGGTTAACT 338
Db 951 GTACCAGCTCCATGGAAGATCTGGCAAGCTCCACAGAGTCCCTGGTGGGTTAACT 1010
QY 339 CCCAGAAAGATCTCATGCTATGCTCAGGGAACCTGATGTGAAACAAGGAGCAAGCA 398
Db 1011 CCCAGAAAGATCTCATGCTATGCTCAGGGAACCTGATGTGAAACAAGGAGCAAGCA 1070
QY 399 AAGAGAGCTGCTCTACATCTGCGCTTGGCAATGGGAATTCAGAGTAGTAACTCGT 458
Db 1071 AAGAGAGCTGCTCTACATCTGCGCTTGGCAATGGGAATTCAGAGTAGTAACTCGT 1130
QY 459 GCTGGACAGAGTGTCAACTTAATGCTTGTGACAAACAAAGAGGAGCACTGTGACAA 518
Db 1131 GCTGGACAGAGTGTCAACTTAATGCTTGTGACAAACAAAGAGGAGCACTGTGACAA 1190
QY 519 GCGGTACATGCCAGAGATGAATGGGTTAAATGTTGCTGGAACATGGCACTGATCC 578

Db 1191 GGCGGTACAATGCCAGGAGATGAATGTCGTTAAATGTTGCTGGAACATGGCACTGATCC 1250
QY 579 AAATATTCAGATGATGAAATACCACTCTACACTATGCTGCTACAAATGAAGATAA 638
Db 1251 AAATATTCAGATGATGAAATACCACTCTACACTATGCTGCTACAAATGAAGATAA 1310
QY 639 ATTAATGCCAAAGCACTGCTTATACGGTGTGATATCGAATCAAAAACACAGCATGG 698
Db 1311 ATTAATGCCAAAGCACTGCTTATACGGTGTGATATCGAATCAAAAACACAGCATGG 1370
QY 699 COTCACCACTGCTACTTGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTAAAT 758
Db 1371 COTCACCACTGCTACTTGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTAAAT 1430
QY 759 CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATATTGC 818
Db 1431 CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATATTGC 1490
QY 819 TGTATGTTGGATCAGCAAGTATAGTCAGCCCTCTACTTTCAGCAAAATGTTGATGATC 878
Db 1491 TGTATGTTGGATCAGCAAGTATAGTCAGCCCTCTACTTTCAGCAAAATGTTGATGATC 1550
QY 879 TTCTCAAGATCTGGAAGAGCGGCGAGAGATGCTGTTTCTAGTCATCATG 933
Db 1551 TTCTCAAGATCTGGAAGAGCGGCGAGAGATGCTGTTTCTAGTCATCATG 1605

RESULT 9

US-08-991-789A-291/c
; Sequence 291, Application US/08991789A
; Patent No. 6225054
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER

NUMBER OF SEQUENCES: 292

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed IP Law Group

STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/991,789A

FILING DATE: 11-Dec-1997

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Potter, Jane E. R.

REGISTRATION NUMBER: 33,332

REFERENCE/DOCKET NUMBER: 210121.419C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 291:

SEQUENCE CHARACTERISTICS:

LENGTH: 1851 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 291:

US-08-991-789A-291

Query Match 87.9%; Score 819.8; DB 3; Length 1851;

Best Local Similarity 99.6%; Pred. No. 2.5e-234;

Matches 832; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy	639	ATTAATGGCCAAAGCACTGCTCTTTATACGGTGTGTATATCGAATCAAAAAACAAGCATGG	639
Db	542	ATTAATGGCCAAAGCACTGCTCTTTATACGGTGTGTATATCGAATCAAAAAACAAGCATGG	483
Qy	699	CCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTTTAAT	758
Db	482	CCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTTTAAT	423
Qy	759	CAAGAAAAAGCGAATTTAAATGCGTGTGATATGGAAGAACTGCTCTCATACTTGC	818
Db	422	CAAGAAAAAGCGAATTTAAATGCGTGTGATATGGAAGAACTGCTCTCATACTTGC	363
Qy	819	TGTATGTTGTGGATCAGCAAGTATAGTTCAGCCCTCTACTTGCACAAAATGTTGATGTATC	878
Db	362	TGTATGTTGTGGATCAGCAAGTATAGTTCAGCCCTCTACTTGCACAAAATGTTGATGTATC	303
Qy	879	TTTCAAGATCTGGAAAGACGGCCAGAGAGTAGTCTGTTTCTAGTCATCATCATG	933
Db	302	TTTCAAGATCTGGAAAGACGGCCAGAGAGTAGTCTGTTTCTAGTCATCATCATG	248
RESULT 15			
US-09-289-198-292/c			
; Sequence 292, Application US/09289198			
; Patent No. 6586570			
; GENERAL INFORMATION:			
; APPLICANT: Frudakis, Tony N.			
; APPLICANT: Smith, John M.			
; APPLICANT: Reed, Steven G.			
; APPLICANT: Misher, Lynda			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE			
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER			
; FILE REFERENCE: 210121.419C5			
; CURRENT APPLICATION NUMBER: US/09/289,198			
; CURRENT FILING DATE: 1999-04-09			
; EARLIER APPLICATION NUMBER: US 09/062,451			
; EARLIER FILING DATE: 1998-04-17			
; EARLIER APPLICATION NUMBER: US 08/991,789			
; EARLIER FILING DATE: 1997-12-11			
; EARLIER APPLICATION NUMBER: US 08/838,762			
; EARLIER FILING DATE: 1997-04-09			
; EARLIER APPLICATION NUMBER: PCT/US97/00485			
; EARLIER FILING DATE: 1997-01-10			
; EARLIER APPLICATION NUMBER: US 08/700,014			
; EARLIER FILING DATE: 1996-08-20			
; EARLIER APPLICATION NUMBER: US 08/585,392			
; EARLIER FILING DATE: 1996-01-01			
; NUMBER OF SEQ ID NOS: 312			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 292			
; LENGTH: 1851			
; TYPE: DNA			
; ORGANISM: Homo sapien			
US-09-289-198-292			
Query Match 87.9%; Score 819.8; DB 4; Length 1851;			
Best Local Similarity 99.6%; Pred. No. 2,Se-234;			
Matches 832; Conservative 0; Mismatches 2; Indels 1; Gaps 1;			
Qy	99	CAGGGGAGCGGCAAGAGCAACTGGGCACTTCTGGAGACCAACAGCACTCCTCTGTGAA	158
Db	1081	CAGGGGAGCGGCAAGAGCAACTGGGCACTTCTGGAGACCAACAGCACTCCTCTGTGAA	1022
Qy	159	GAGCCTTGGAGCAAGGTGCAAGTGGTCTGCCACTGTTTCCCTGTGAGGGGAG	218
Db	1021	GACGCTTGGAGCAAGAGGTGCAAGTGGTCTGCCACTGTTTCCCTGTGCA-GGGGAG	963
Qy	219	CGCAGAGCAACGTGGCGCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCAG	278
Db	962	CGCAGAGCAACGTGGTCCCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCAG	903
Qy	279	GTACCAAGCTCCATGGAGAGATCTGACCAAGCTCCACAGAGCTCCCTGGTGGGGTAAAGT	338

Db	902	GTACCACGTCCTGAGAGATCTGGACAAAGCTCCACAGAGCTGCTGGTGGGTAAAGT	843
Qy	339	CCCCAGAAAGGATCTCATCTCATCTCAGGACACTGATGTGAACAGAGGACAGCA	398
Db	842	CCCCAGAAAGGATCTCATCTCATCTCAGGACACTGATGTGAACAGAGGACAGCA	783
Qy	399	AAAGAGGACTGCTCTACATCTGGCCCTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCGT	458
Db	782	AAAGAGGACTGCTCTACATCTGGCCCTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCGT	723
Qy	459	GCTGCACAGACGATCTCACTTAATGTCTTCACACAAAGAGGACAGCTCTGACAAA	518
Db	722	GCTGCACAGACGATCTCACTTAATGTCTTCACACAAAGAGGACAGCTCTGACAAA	663
Qy	519	GGCCGTACAATGCCAGGAAGATGAATGTCGTTAATGTTGCTGGAACAATGCCACTGATCC	578
Db	662	GGCCGTACAATGCCAGGAAGATGAATGTCGTTAATGTTGCTGGAACAATGCCACTGATCC	603
Qy	579	AAATATTCAGATGATGGAATACCACTCTACACTATGCTGTCTACAAATGAAGATAA	638
Db	602	AAATATTCAGATGATGGAATACCACTCTACACTATGCTGTCTACAAATGAAGATAA	543
Qy	639	ATTAATGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG	698
Db	542	ATTAATGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG	483
Qy	699	CCTCACACACTGCTACTTGGTATACATGAGCAAAAAACAAGGTGGTGAATTTTAAAT	758
Db	482	CCTCACACACTGCTACTTGGTATACATGAGCAAAAAACAAGGTGGTGAATTTTAAAT	423
Qy	759	CAAGAAAAAGCGAATTTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATACTGC	818
Db	422	CAAGAAAAAGCGAATTTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATACTGC	363
Qy	819	TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGATC	878
Db	362	TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGATC	303
Qy	879	TTCCTCAGATCTGGAAGACCGCCAGAGATGCTCTTTCTAGTCATCATCTG	933
Db	302	TTCCTCAGATCTGGAAGACCGCCAGAGATGCTCTTTCTAGTCATCATCTG	248

Search completed: April 30, 2004, 13:09:24
Job time : 99 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: April 30, 2004, 10:11:56 ; Search time 3748 Seconds
(without alignments)
10789.501 Million cell updates/sec
Title: US-10-079-137B-343
Perfect score: 933
Sequence: 1 atgggtggtgaggttgattc.....tggtttcagtcacatcatg 933
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.ov.*
22: em.pat.*
23: em.ph.*
24: em.pl.*
25: em.ro.*
26: em.sts.*
27: em.un.*
28: em.vi.*
29: em.vi.*
30: em.htg.hum.*
31: em.htg.inv.*
32: em.htg.other.*
33: em.htg.mus.*
34: em.htg.pln.*
35: em.htg.rod.*
36: em.htg.mam.*
37: em.htg.vrt.*
38: em.sv.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	831.8	89.2	879	6	AR261059 Sequence
2	831.8	89.2	879	6	AR278590 Sequence
3	831.8	89.2	879	6	AR367286 Sequence
4	831.8	89.2	879	6	AR400322 Sequence
5	831.8	89.2	879	6	AR405589 Sequence
6	831.8	89.2	879	6	AR433323 Sequence
7	831.8	89.2	879	6	AX141041 Sequence
8	831.8	89.2	879	6	AX200901 Sequence
9	831.8	89.2	879	6	AX267557 Sequence
10	831.8	89.2	879	6	AX316977 Sequence
11	831.8	89.2	1852	6	AR261058 Sequence
12	831.8	89.2	1852	6	AR278589 Sequence
13	831.8	89.2	1852	6	AR367285 Sequence
14	831.8	89.2	1852	6	AR400321 Sequence
15	831.8	89.2	1852	6	AR405588 Sequence
16	831.8	89.2	1852	6	AR433322 Sequence
17	831.8	89.2	1852	6	AX141040 Sequence
18	831.8	89.2	1852	6	AX200900 Sequence
19	831.8	89.2	1852	6	AX267556 Sequence
20	831.8	89.2	1852	6	AX282954 Sequence
21	831.8	89.2	1852	6	AX316976 Sequence
22	819.8	87.9	1851	6	AR148112 Sequence
23	819.8	87.9	1851	6	BD242264 Compounds
24	819.8	87.9	1851	6	AR260940 Sequence
25	819.8	87.9	1851	6	AR278471 Sequence
26	819.8	87.9	1851	6	AR350934 Sequence
27	819.8	87.9	1851	6	AR350935 Sequence
28	819.8	87.9	1851	6	AR367167 Sequence
29	819.8	87.9	1851	6	AR371063 Sequence
30	819.8	87.9	1851	6	AR400203 Sequence
31	819.8	87.9	1851	6	AR405470 Sequence
32	819.8	87.9	1851	6	AR433310 Sequence
33	819.8	87.9	1851	6	AR433311 Sequence
34	819.8	87.9	1851	6	AX106585 Sequence
35	819.8	87.9	1851	6	AX140876 Sequence
36	819.8	87.9	1851	6	AX200736 Sequence
37	819.8	87.9	1851	6	AX267392 Sequence
38	819.8	87.9	1851	6	AX282952 Sequence
39	819.8	87.9	1851	6	AX316954 Sequence
40	819.8	87.9	1851	6	AX316955 Sequence
41	819.8	87.9	1851	6	BD084487 Compositi
42	819.8	87.9	1851	6	BD084488 Compositi
43	819.8	87.9	2184	6	BD242268 Compounds
44	819.8	87.9	2184	6	AR260944 Sequence
45	819.8	87.9	2184	6	AR278475 Sequence

ALIGNMENTS

RESULT 1
AR261059
LOCUS AR261059
DEFINITION Sequence 531 from patent US 6321716.
ACCESSION AR261059
VERSION AR261059.1 GI:28071822
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 879)
Mashiki, Z. and Harada, J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: US 6321716-A 531 27-NOV-2001;
FEATURES Location/Qualifiers

linear PAT 29-JAN-2003

Pred. No. is the number of results predicted by chance to have a

Db	642	CCTCACACAC	TGCTACTTGGTATACATGAGCAAAACAGCAAGTGGTGAATTTTAAT	701
Qy	759	CAAGAAAAAGCGAA	TTTAAATGCGCTGGATAGATATGGAAGACTGCTCTCATATTGC	818
Db	702	CAAGAAAAAGCGAA	TTTAAATGCGCTGGATAGATATGGAAGACTGCTCTCATATTGC	761
Qy	819	TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAAGCAAAATGTTGATCTATC	878	
Db	762	TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAAGCAAAATGTTGATCTATC	821	
Qy	879	TTCTCAAGATCTGGAAGACGGCCAGAGAGTAGTGTCTTTCTAGTCATCATCATG	933	
Db	822	TTCTCAAGATCTGGAAGACGGCCAGAGAGTAGTGTCTTTCTAGTCATCATCATG	876	
RESULT 4				
AR400322				
LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
FEATURES				
source				
ORIGIN				
Query Match				
Best Local Similarity				
Matches				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				
Qy				
Db				

Db 462 GCGCTACATGCGAGAGATGATGCGTTATGTTGCTGACATGGCACTGATCC 521
Qy 579 AATATTCAGATGAGATGGAATACCACTCCTACACTATGCTGTCTACATGAAGATAA 638
Db 522 AATATTCAGATGAGATGGAATACCACTCCTACACTATGCTGTCTACATGAAGATAA 581
Qy 639 ATTAATGCGCAAGACACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 698
Db 582 ATTAATGCGCAAGACACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 641
Qy 699 CTTACACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTAAAT 758
Db 642 CTTACACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTAAAT 701
Qy 759 CAGAAAAAGCGAATTTAAATGCGTGGATAGATATGGAAGAAGTCTCTCATATTCG 818
Db 702 CAGAAAAAGCGAATTTAAATGCGTGGATAGATATGGAAGAAGTCTCTCATATTCG 761
Qy 819 TGTATGTTGGATCAGCAAGTATGATGAGCCCTCTACTTTGAGCAAAATGTTGATGATC 878
Db 762 TGTATGTTGGATCAGCAAGTATGATGAGCCCTCTACTTTGAGCAAAATGTTGATGATC 821
Qy 879 TTCTCAAGATCTGGAAGACGGCCAGAGATGCTGTTCTAGTCATCATCATG 933
Db 822 TTCTCAAGATCTGGAAGACGGCCAGAGATGCTGTTCTAGTCATCATCATG 876

RESULT 5
AR405589
LOCUS AR405589 879 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 531 from patent US 6630305.
ACCESSION AR405589
VERSION AR405589.1 GI:40154426
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 879)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6630305-A 531 07-OCT-2003;
FEATURES Location/Qualifiers
source 1..879
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 89.2%; Score 831.8; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 7.4e-196;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 99 CAGGGGAGCGGCAAGACGACGTTCTGGAGACCAACACACTCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGACGACGTTCTGGAGACCAACACACTCTCTGTGAA 101
Qy 159 GACGCTTGGAGCAAGAGTGCATGCTGCTGCTCCCTGCTGAGGGGAG 218
Db 102 GACGCTTGGAGCAAGAGTGCATGCTGCTGCTCCCTGCTGAGGGGAG 161
Qy 219 CGGCAAGACCAAGTGGCGCTTGGGAGACTAGATCAGCGCCCTTCATGATCCAG 278
Db 162 CGGCAAGACCAAGTGGCGCTTGGGAGACTAGATCAGCGCCCTTCATGATCCAG 221
Qy 279 GTACCACCTCCATGAGAGATCTGGCAAGCTCCACAGAGCTGCTGGTGGGTAAGT 338
Db 222 GTACCACCTCCATGAGAGATCTGGCAAGCTCCACAGAGCTGCTGGTGGGTAAGT 281
Qy 339 CCCAGAAAGGATCTCATGCTCAGGACACTGATGTGAACAAGAGGACAGCA 398

Db 282 CCCAGAAAGGATCTCATGCTCAGGACACGGATGTGAACAAGAGGACAGCA 341
Qy 339 AAAGAGGACTCTCTACATCTGGCTCTGCAATGGGAATTCAGAAGTGTAAACCTCGT 458
Db 342 AAAGAGGACTCTCTACATCTGGCTCTGCAATGGGAATTCAGAAGTGTAAACCTCGT 401
Qy 459 GCTGACAGAGCGATGTCAACTTAATGCTCTTGAACAACAAGAGGACAGCTCTGACAAA 518
Db 402 GCTGACAGAGCGATGTCAACTTAATGCTCTTGAACAACAAGAGGACAGCTCTGACAAA 461
Qy 519 GCGCGTCAATGCCAGGAGATGAATGCGTTAATGTTGCTGGAACATGCGACTGATCC 578
Db 462 GCGCGTCAATGCCAGGAGATGAATGCGTTAATGTTGCTGGAACATGCGACTGATCC 521
Qy 579 AATATTTCCAGATGAGTATGGAATACCACTCTACACTATGCTCTACATGAAGATAA 638
Db 522 AATATTTCCAGATGAGTATGGAATACCACTCTACACTATGCTCTACATGAAGATAA 581
Qy 639 ATTAATGCGCAAGACACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 698
Db 582 ATTAATGCGCAAGACACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 641
Qy 699 CTTACACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTAAAT 758
Db 642 CTTACACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTAAAT 701
Qy 759 CAGAAAAAGCGAATTTAAATGCGTGGATAGATATGGAAGAAGTCTCTCATATTCG 818
Db 702 CAGAAAAAGCGAATTTAAATGCGTGGATAGATATGGAAGAAGTCTCTCATATTCG 761
Qy 819 TGTATGTTGGATCAGCAAGTATGATGAGCCCTCTACTTTGAGCAAAATGTTGATGATC 878
Db 762 TGTATGTTGGATCAGCAAGTATGATGAGCCCTCTACTTTGAGCAAAATGTTGATGATC 821
Qy 879 TTCTCAAGATCTGGAAGACGGCCAGAGATGCTGTTCTAGTCATCATCATG 933
Db 822 TTCTCAAGATCTGGAAGACGGCCAGAGATGCTGTTCTAGTCATCATCATG 876

RESULT 6
AR433323
LOCUS AR433323 879 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 314 from patent US 6656480.
ACCESSION AR433323
VERSION AR433323.1 GI:40196105
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 879)
AUTHORS Retter,M.W. and Dillon,D.C.
TITLE Compositions and methods for the treatment and diagnosis of breast cancer
JOURNAL Patent: US 6656480-A 314 02-DEC-2003;
FEATURES Location/Qualifiers
source 1..879
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 89.2%; Score 831.8; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 7.4e-196;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 99 CAGGGGAGCGGCAAGACGTTCTGGAGACCAACACACTCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGACGTTCTGGAGACCAACACACTCTCTGTGAA 101
Qy 159 GACGCTTGGAGCAAGAGTGCATGCTGCTGCTCCCTGCTGAGGGGAG 218
Db 102 GACGCTTGGAGCAAGAGTGCATGCTGCTGCTCCCTGCTGAGGGGAG 161

Qy	219	CGCGAAGAGCAACGTGGCGCGCTTGGGAGACTACGATGACAGCGCCTTANTGATCCGAC	278
Db	162	CGCGAAGAGCAACGTGGTTCGCTTGGGAGACTACGATGACAGCGCCTTATGGATCCGAC	221
Qy	279	GTACACAGTCCTCATGTGAGAAAGACTCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGTAAAGT	338
Db	222	GTACCAAGTCATGTGAGAAAGACTCTGGERCAAGCTCCAAGAGCTGCCTGGTGGGGTAAAGT	281
Qy	339	CCCCGAAAAGGATCTCATCTGTCATGCTCAGGGAACACTGATGTGAAACAAGAGGACAAGCA	398
Db	282	CCCCGAAAAGGATCTCATCTGTCATGCTCAGGGAACACGGATGTGAAACAAGAGGACAAGCA	341
Qy	399	AAAGAGGACTGCTCTACACTCTGGCCTCTGCCAATGGGAAATTACAGAGTAGTAAACTCTGT	458
Db	342	AAAGAGGACTGCTCTACACTCTGGCCTCTGCCAATGGGAAATTACAGAGTAGTAAACTCTGT	401
Qy	459	GCTGGACAGACGATGTCAACTTAATGTCTTTGACAACAACAAAAGAGGACAGCTCTGCAAA	518
Db	402	GCTGGACAGACGATGTCAACTTAATGTCTTTGACAACAACAAAAGAGGACAGCTCTGCAAA	461
Qy	519	GGCGGTACAACTCCAGGAGAGATGAATGTCCTTAATGTCCTGGACATGGCACTGATCC	578
Db	462	GGCGGTACAACTCCAGGAGAGATGAATGTCCTTAATGTCCTGGACATGGCACTGATCC	521
Qy	579	AAATATTCAGATGAGTAGTGGAAATPACCACTCTACACTATGCTGTCTACAAATGAAGATAA	638
Db	522	AAATATTCAGATGAGTAGTGGAAATPACCACTCTACACTATGCTGTCTACAAATGAAGATAA	581
Qy	639	ATTATGGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAGCATGG	698
Db	582	ATTATGGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAGCATGG	641
Qy	699	CCTCACACCACTGCTACTTGGTATATACATGAGCAAAAAACAGCAAGTGGTGAATTTTTAAT	758
Db	642	CCTCACACCACTGCTACTTGGTATATACATGAGCAAAAAACAGCAAGTGGTGAATTTTTAAT	701
Qy	759	CAAGAAAAAAGCGAATTTTAATGCGCTGGATAGATATGGAAGAAACTGCTCTCATCTTGC	818
Db	702	CAAGAAAAAAGCGAATTTTAATGCGCTGGATAGATATGGAAGAAACTGCTCTCATCTTGC	761
Qy	819	TGPTATCTGTGGATCAGCAAGTATAGTCAGCGCCTCTACTTGGACAAAGTGTTCATGTATC	878
Db	762	TGPTATCTGTGGATCAGCAAGTATAGTCAGCGCCTCTACTTGGACAAAGTGTTCATGTATC	821
Qy	879	TTCTCAAGATCTGGAAGACGCGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG	933
Db	822	TTCTCAAGATCTGGAAGACGCGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG	876

RESULT 7			
AX141041			
LOCUS	AX141041	879 bp	DNA
DEFINITION	Sequence 531 from Patent WO0134802.		linear
			PAT 31-MAY-2001

AA141041.1	GI:114281098
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[illegible][illegible]

Db 582 ATTAATGCCAAAGCAGCTGCTCTTATACGGTGTGATATCGAATCAAAAACAAGCATGG 641
Qy 699 CCTCACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGTGAAATTTTAAAT 758
Db 642 CCTCACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGTGAAATTTTAAAT 701
Qy 759 CAAGAAAACGCAATTTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC 818
Db 702 CAAGAAAACGCAATTTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC 761
Qy 819 TGTATGTTGGATCAGCAAGTATAGTACGCCCTCTACTTGGCAAAATGTTGATGATC 878
Db 762 TGTATGTTGGATCAGCAAGTATAGTACGCCCTCTACTTGGCAAAATGTTGATGATC 821
Qy 879 TTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTCTAGTCATCATG 933
Db 822 TTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTCTAGTCATCATG 876

RESULT 10
AX316977
LOCUS AX316977 879 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 314 from Patent W00190152.
ACCESSION AX316977
VERSION AX316977.1 GI:17900048
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Frudakis,T.N., Reed,S.G., Smith,J.M., Misher,L.E., Dillon,D.C., Retter,M.W., Wang,A., Skeiky,Y.A., Harlocker,S.L. and Day,C.H.
JOURNAL Compositions and methods for the therapy and diagnosis of breast cancer
PATENT: WO 0190152-A 314 29-NOV-2001;
CORIXA CORPORATION (US)
FEATURES
LOCATION/Qualifiers
SOURCE 1..879
ORGANISM="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 89.2%; Score 831.8; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 7.4e-196;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 99 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTTGGAGACCACACGACTCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTTGGAGACCACACGACTCTCTGTGAA 101
Qy 159 GACGCTTGGAGCAAGAGGTGCAAGTGGTCTGCCACTGCTTCCCTGCTGCAAGGGGAG 218
Db 102 GACGCTTGGAGCAAGAGGTGCAAGTGGTCTGCCACTGCTTCCCTGCTGCAAGGGGAG 161
Qy 219 CGGCAAGAGCAACGTGGGCGCTTGGGAGACTACGATGACAGCGCTTTCATGGATCCCAG 278
Db 162 CGGCAAGAGCAACGTGGTCTGCTTGGGAGACTACGATGACAGCGCTTTCATGGATCCCAG 221
Qy 279 GTACCCAGTCCATGGAGAGATCTGCAAGCTCCACAGAGCTGCTTGGGGTAAAGT 338
Db 222 GTACCCAGTCCATGGAGAGATCTGCAAGCTCCACAGAGCTGCTTGGGGTAAAGT 281
Qy 339 CCCAGAAAGGATCTCATCTGCTCAGGGACATGATGTGAACAGAGGGGCAAGCA 398
Db 282 CCCAGAAAGGATCTCATCTGCTCAGGGACATGATGTGAACAGAGGGGCAAGCA 341
Qy 399 AAAGAGACTGCTCTACATCTGCGCTTGCCTTGGCAATGGGAATTCAGAAAGTAGTAAACTCGT 458
Db 342 AAAGAGACTGCTCTACATCTGCGCTTGCCTTGGCAATGGGAATTCAGAAAGTAGTAAACTCGT 401
Qy 459 GCTGGACAGACGATGTCAACTTAAATGCTTGTGACAAAAAGAGGACAGCTCTGACAAA 518

Db 402 GCTGGACAGACGATGTCACTTAAATGCTTGGACAAACAAAAGAGACAGCTCTGACAAA 461
Qy 519 GGCCTGACCAATCCAGGAAGATGAATGTCGCTTAAATGTTGCTGGAACATGGCACTGATCC 578
Db 462 GGCCTGACCAATCCAGGAAGATGAATGTCGCTTAAATGTTGCTGGAACATGGCACTGATCC 521
Qy 579 AAATATTCAGATGAGTATGGAATACCACTTACACTATGCTGCTCAATGAAGATAA 638
Db 522 AAATATTCAGATGAGTATGGAATACCACTTACACTATGCTGCTCAATGAAGATAA 581
Qy 639 ATTAATGGCCAAAGCACTGCTCTTATAGCGTCTGATATCGAATCAAAAAACAAGCATGG 698
Db 582 ATTAATGGCCAAAGCACTGCTCTTATAGCGTCTGATATCGAATCAAAAAACAAGCATGG 641
Qy 699 CTTACACCACTGCTACTTGGTATACATGACAAAAACAGCAAGTGGTGAATTTTAAAT 758
Db 642 CTTACACCACTGCTACTTGGTATACATGACAAAAACAGCAAGTGGTGAATTTTAAAT 701
Qy 759 CAAGAAAAAGCGAAATTTAAATGCGCTCGATATGATATGGAAGAACTGCTCTCATCTTGC 818
Db 702 CAAGAAAAAGCGAAATTTAAATGCGCTCGATATGATATGGAAGAACTGCTCTCATCTTGC 761
Qy 819 TGTATGTTGGATCAGCAAGTATAGTACGCCCTCTACTTGGCAAAATGTTGATGATC 878
Db 762 TGTATGTTGGATCAGCAAGTATAGTACGCCCTCTACTTGGCAAAATGTTGATGATC 821
Qy 879 TTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTCTAGTCATCATG 933
Db 822 TTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTCTAGTCATCATG 876

RESULT 11
AR261058
LOCUS AR261058 1852 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 530 from patent US 6321716.
ACCESSION AR261058
VERSION AR261058.1 GI:28071821
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1852)
AUTHORS Mashiki,Z. and Harada,J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: US 6321716-A 530 27-NOV-2001;
FEATURES Location/Qualifiers
SOURCE 1..1852
ORGANISM="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 89.2%; Score 831.8; DB 6; Length 1852;
Best Local Similarity 99.8%; Pred. No. 7.4e-196;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 99 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTTGGAGACCACACGACTCTCTGTGAA 158
Db 771 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTTGGAGACCACACGACTCTCTGTGAA 830
Qy 159 GACGCTTGGAGCAAGAGGTGCAAGTGGTCTGCCACTGCTTCCCTGCTGCAAGGGGAG 218
Db 831 GACGCTTGGAGCAAGAGGTGCAAGTGGTCTGCCACTGCTTCCCTGCTGCAAGGGGAG 890
Qy 219 CGGCAAGAGCAACGTGGGCGCTTGGGAGACTACGATGACAGCGCTTTCATGGATCCCAG 278
Db 891 CGGCAAGAGCAACGTGGTCTGCTTGGGAGACTACGATGACAGCGCTTTCATGGATCCCAG 950
Qy 279 GTACCCAGTCCATGGAGAGATCTGGAAGCTCCACAGAGCTGCTTGGGGTAAAGT 338
Db 951 GTACCCAGTCCATGGAGAGATCTGGAAGCTCCACAGAGCTGCTTGGGGTAAAGT 1010
Qy 339 CCCAGAAAGGATCTCATCTGCTCAGGGACACTGATGTGAACAGAGGGGCAAGCA 398

Db 1011 CCCCAGAAAGGATCTCATCGTCATGCTCAGGACACCGGATGTAACAAGAGGGAACAAGCA 1070
Qy 399 AAAGAGGAGCTGCTTACATCTGGCCCTCTGCCAATGGGAATTCAGAAAGTAGTAAATCGT 458
Db 1071 AAAGAGGAGCTGCTTACATCTGGCCCTCTGCCAATGGGAATTCAGAAAGTAGTAAATCGT 1130
Qy 459 GGTGACAGACGATGTCACTTAATGTCTTGAACAACAAAAGAGGACAGCTCTGACAAA 518
Db 1131 GGTGACAGACGATGTCACTTAATGTCTTGAACAACAAAAGAGGACAGCTCTGACAAA 1190
Qy 519 GGCCTGTACAATCCAGGAAGATGAATGCGTTAATGTGTGGAACATGCACTGATCC 578
Db 1191 GGCCTGTACAATCCAGGAAGATGAATGCGTTAATGTGTGGAACATGCACTGATCC 1250
Qy 579 AAATATTCAGATAGTATGGAATATACATCTACATGATGTGTCTCAATAGAGATAA 638
Db 1251 AAATATTCAGATAGTATGGAATATACATCTACATGATGTGTCTCAATAGAGATAA 1310
Qy 639 ATTAATGCGCAAGCACTGCTTATACGCTGCTGATATCGAATCAAAAAACAAGCATGG 698
Db 1311 ATTAATGCGCAAGCACTGCTTATACGCTGCTGATATCGAATCAAAAAACAAGCATGG 1370
Qy 699 CTTACACCACTGCTACTTGTGATATACATGACGCAAAAAACAGCAAGTGTGAAATTTTAA 758
Db 1371 CTTACACCACTGCTACTTGTGATATACATGACGCAAAAAACAGCAAGTGTGAAATTTTAA 1430
Qy 759 CAAGAAAAGCGAATTTAAATGCGCTGATAGATGGAAGATGCTCTCATATGTC 818
Db 1431 CAAGAAAAGCGAATTTAAATGCGCTGATAGATGGAAGATGCTCTCATATGTC 1490
Qy 819 TGTATGTTGTGGATCAGCAAGATATAGTCAGCCCTCTACTTGAGCAAAATGTTGATATC 878
Db 1491 TGTATGTTGTGGATCAGCAAGATATAGTCAGCCCTCTACTTGAGCAAAATGTTGATATC 1550
Qy 879 TTCTCAAGATCTGGAAGCGCCAGAGATATGCTGTTCTAGTCATCATCATG 933
Db 1551 TTCTCAAGATCTGGAAGCGCCAGAGATATGCTGTTCTAGTCATCATCATG 1605

RESULT 12
AR278589
LOCUS AR278589 1852 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 530 from patent US 6512094.
ACCESSION AR278589
VERSION AR278589.1 GI:29712835
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1852)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedwick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate Cancer
JOURNAL Patent: US 6512094-A 530 28-JAN-2003;
FEATURES Location/Qualifiers
source 1..1852
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 89.2%; Score 831.8; DB 6; Length 1852;
Best Local Similarity 99.8%; Pred. No. 7.4e-196;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 99 CAGGGGAGCGGCAAGAGCAAGTGGGCACTCTGAGACCAACAGCACTCTCTGTGAA 158
Db 771 CAGGGGAGCGGCAAGAGCAAGTGGGCACTCTGAGACCAACAGCACTCTCTGTGAA 830
Qy 159 GAGCGTTGGAGCAAGAGTGCAGTGGTGTGCTGCCACTGCTCCCTGCTGCGAGGGGAG 218

Db 831 GAGCGTTGGAGCAAGAGTGCAGTGGTGTGCTGCCACTCTCCCTGCTGAGGGGAG 890
Qy 219 CGGCAAGAGCAACGCTGGCGCTTGGGGAGACTACGATGACAGCGCTTTCATGATCCCCAG 278
Db 891 CGGCAAGAGCAACGCTGGTGGTGGGAGACTACGATGACAGCGCTTTCATGATCCCCAG 950
Qy 279 GTACCAAGCTCCATGGAGAGATCTGGAAGCTTCCACAGAGCTGCTGCTGGGTAAAGT 338
Db 951 GTACCAAGCTCCATGGAGAGATCTGGAAGCTTCCACAGAGCTGCTGCTGGGTAAAGT 1010
Qy 339 CCCAGAAAGGATCTCATGCTCATGCTCAGGACACCTGATGTGAAACAAGAGGGAACAAGCA 398
Db 1011 CCCAGAAAGGATCTCATGCTCATGCTCAGGACACCTGATGTGAAACAAGAGGGAACAAGCA 1070
Qy 399 AAAGAGGAGCTGCTTACATCTGGCCCTCTGCCAATGGGAATTCAGAAAGTAGTAAATCGT 458
Db 1071 AAAGAGGAGCTGCTTACATCTGGCCCTCTGCCAATGGGAATTCAGAAAGTAGTAAATCGT 1130
Qy 459 GCTGGACAGACGATGTCACTTAATGTCTTGAACAACAAAAGAGGACAGCTCTGACAAA 518
Db 1131 GCTGGACAGACGATGTCACTTAATGTCTTGAACAACAAAAGAGGACAGCTCTGACAAA 1190
Qy 519 GGCCTGTACAATCCAGGAAGATGAATGCGTTAATGTGTGGAACATGCACTGATCC 578
Db 1191 GGCCTGTACAATCCAGGAAGATGAATGCGTTAATGTGTGGAACATGCACTGATCC 1250
Qy 579 AAATATTCAGATAGTATGGAATATACATCTACATGATGTGTCTCAATAGAGATAA 638
Db 1251 AAATATTCAGATAGTATGGAATATACATCTACATGATGTGTCTCAATAGAGATAA 1310
Qy 639 ATTAATGCGCAAGCACTGCTTATACGCTGCTGATATCGAATCAAAAAACAAGCATGG 698
Db 1311 ATTAATGCGCAAGCACTGCTTATACGCTGCTGATATCGAATCAAAAAACAAGCATGG 1370
Qy 699 CTTACACCACTGCTACTTGTGATATACATGACGCAAAAAACAGCAAGTGTGAAATTTTAA 758
Db 1371 CTTACACCACTGCTACTTGTGATATACATGACGCAAAAAACAGCAAGTGTGAAATTTTAA 1430
Qy 759 CAAGAAAAGCGAATTTAAATGCGCTGATAGATGGAAGATGCTCTCATATGTC 818
Db 1431 CAAGAAAAGCGAATTTAAATGCGCTGATAGATGGAAGATGCTCTCATATGTC 1490
Qy 819 TGTATGTTGTGGATCAGCAAGATATAGTCAGCCCTCTACTTGAGCAAAATGTTGATATC 878
Db 1491 TGTATGTTGTGGATCAGCAAGATATAGTCAGCCCTCTACTTGAGCAAAATGTTGATATC 1550
Qy 879 TTCTCAAGATCTGGAAGCGCCAGAGATATGCTGTTCTAGTCATCATCATG 933
Db 1551 TTCTCAAGATCTGGAAGCGCCAGAGATATGCTGTTCTAGTCATCATCATG 1605

RESULT 13
AR367285
LOCUS AR367285 1852 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 530 from patent US 6329505.
ACCESSION AR367285
VERSION AR367285.1 GI:34600260
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1852)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Yu, J., Reed, S.G., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A. and Day, C.H.
TITLE Compositions and methods for therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6329505-A 530 11-DEC-2001;
FEATURES Location/Qualifiers
source 1..1852
/organism="unknown"
/mol_type="genomic DNA"

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 10:10:26 ; Search time 426 Seconds
(without alignments)
9304.152 Million cell updates/sec

Title: US-10-079-137B-343

Perfect score: 933

Sequence: 1 atggtggttaggttgattc.....tggtttctagcatcatcatg 933

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001as.*
- 5: Geneseq2001bs.*
- 6: Geneseq2002s.*
- 7: Geneseq2003as.*
- 8: Geneseq2003bs.*
- 9: Geneseq2003cs.*
- 10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	933	100.0	933	9	ADC15395 Human bre
2	913.8	97.9	939	9	ADC15396 Human bre
3	864.2	92.6	1689	8	ABT43733 Molecule
4	835	89.5	876	9	ADC15394 Human bre
5	831.8	88.2	876	9	ADC15393 Human bre
6	831.8	88.2	879	3	AAC81016 Human bre
7	831.8	88.2	879	4	AAS63919 Human pro
8	831.8	88.2	879	4	AAS63919 Human pro
9	831.8	88.2	879	5	ACA59727 Prostate
10	831.8	88.2	879	5	ACA59727 Prostate
11	831.8	88.2	879	6	ABL95290 Human B30
12	831.8	88.2	879	6	AAS9862 Breast tu
13	831.8	88.2	879	7	ADC95454 Prostate
14	831.8	88.2	879	7	ADA11393 Human bre
15	831.8	88.2	879	9	ADC15366 Human bre
16	831.8	88.2	879	9	ADB13981 Human pro
17	831.8	88.2	1852	3	AAC81015 Human bre
18	831.8	88.2	1852	4	AAS93825 Human pro
19	831.8	88.2	1852	4	AAH93825 Human pro
20	831.8	88.2	1852	4	AAH93825 Human pro
21	831.8	88.2	1852	4	AAH85139 Human pro
22	831.8	88.2	1852	5	ACA59726 Prostate
23	831.8	88.2	1852	6	ABL95289 Human B30

ALIGNMENTS

RESULT 1

ADC15395	ADCL15395 standard; DNA; 933 BP.
ID	ADCL15395 standard; DNA; 933 BP.
XX	XX
AC	ADC15395;
XX	XX
DT	18-DEC-2003 (first entry)
XX	XX
DE	Human breast tumour protein DNA, SEQ ID 343.
XX	XX
KW	Cytostatic; Gene therapy; breast cancer; breast tumour protein; human; ds.
KW	ds.
XX	XX
CS	Homo sapiens.
XX	XX
FN	WO2003013431-A2.
XX	XX
PD	20-FEB-2003.
XX	XX
PF	05-AUG-2002; 2002WO-US024917.
XX	XX
PR	07-AUG-2001; 2001US-00924400.
PR	20-FEB-2002; 2002US-00079137.
PR	02-AUG-2002; 2002US-00212679.
XX	(CORI-) CORIXA CORP.
XX	Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH; Kalos MD;
XX	WPI; 2003-342398/32.
XX	New polynucleotide, useful for preparing a composition for diagnosing, treating or preventing cancer.
XX	Claim 1; SEQ ID NO 343; 308pp; English.
XX	The present invention relates to compositions and methods for the therapy and diagnosis of cancer, particularly breast cancer. The method for detecting the presence of a cancer in a patient comprises: obtaining a biological sample from the patient; contacting the biological sample with a binding agent that binds to the polypeptide; detecting in the sample an amount of the polypeptide that binds to the binding agent; and comparing the amount of the polypeptide to a predetermined cut-off value. Treating breast cancer comprises administering a composition comprising breast tumour proteins and nucleic acids, which simulates and/or expands T cells

AAS99861 Breast tu
ACC95453 Prostate
ADA11392 Human bre
ADCL15365 Human pro
ADBL3980 Human bre
AAV68992 DNA molec
AAS68993 DNA molec
AAH6531 Human imm
AAC81004 Human B11
AAC81003 Human bre
AAH93707 Human pro
AAH67209 B305D iso
AAS63800 Human pro
AAH02772 Prostate
AAH5021 Human pro
ACA95608 Prostate
AB195171 Human B30
AAS99850 Breast tu
AAS99849 Breast tu
ABK46893 Human bre
ABK46894 Human bre
ACC95335 Prostate

CC specific for the tumour protein. The present sequence was used to
XX illustrate the invention.

SQ Sequence 933 BP; 272 A; 201 C; 248 G; 212 T; 0 U; 0 Other;

Query Match 100.0%; Score 933; DB 9; Length 933;
Best Local Similarity 100.0%; Pred. No. 6.3e-269;
Matches 933; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGGTGGTTGAGTTGATTCATGCGCGGTGCTCTTCTGTGAAGAGCCATTGGTCTC 60
Dd 1 ATGGTGGTTGAGTTGATTCATGCGCGGTGCTCTTCTGTGAAGAGCCATTGGTCTC 60
QY 61 AGGAGCAAGATGGCGCAAGTGGTCTCTTCCCTGCTGAGGGGAGCGGCAAGAGCAAC 120
Dd 61 AGGAGCAAGATGGCGCAAGTGGTCTCTTCCCTGCTGAGGGGAGCGGCAAGAGCAAC 120
QY 121 GTGGGCACTTCTGGAGACCAACAGCTCTCTGTGAAGACGCTTGGGAGCAAGAGTGC 180
Dd 121 GTGGGCACTTCTGGAGACCAACAGCTCTCTGTGAAGACGCTTGGGAGCAAGAGTGC 180
QY 181 AATGGTGTCTGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGCAAGTGGCGCT 240
Dd 181 AATGGTGTCTGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGCAAGTGGCGCT 240
QY 241 TGGGGAGCTACGATGACAGCGCTTCCAGTACCAGTACCAGTCCATGAGAGAT 300
Dd 241 TGGGGAGCTACGATGACAGCGCTTCCAGTACCAGTACCAGTCCATGAGAGAT 300
QY 301 CTGAGCAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAAGAGGATCTCATCTC 360
Dd 301 CTGAGCAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAAGAGGATCTCATCTC 360
QY 361 ATGCTCAGGACACTGATGTGAACAAGAGGCAAGCAAGCAAGAGGACTGCTCTACATCTG 420
Dd 361 ATGCTCAGGACACTGATGTGAACAAGAGGCAAGCAAGCAAGAGGACTGCTCTACATCTG 420
QY 421 GCCTCTGCCAATGGGATTCAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 480
Dd 421 GCCTCTGCCAATGGGATTCAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 480
QY 481 AATGTCTCTGACAAACAAAGAGGACAGCTCTGACAAAGGCGGTACAAATGCCAGGAAGAT 540
Dd 481 AATGTCTCTGACAAACAAAGAGGACAGCTCTGACAAAGGCGGTACAAATGCCAGGAAGAT 540
QY 541 GAATGTGCGTTAATGTTGCTGGAACATGGACATGATCCAAATATTCAGATGATGGA 600
Dd 541 GAATGTGCGTTAATGTTGCTGGAACATGGACATGATCCAAATATTCAGATGATGGA 600
QY 601 AATACCACTCTACATGCTGTCTACATGAAGTAAATTAATGCCAAAGCACTGCTC 660
Dd 601 AATACCACTCTACATGCTGTCTACATGAAGTAAATTAATGCCAAAGCACTGCTC 660
QY 661 TTATACGGTCTGATATCGAATCAAAAAAAGATGCGCTCACACCACTGCTACTTGT 720
Dd 661 TTATACGGTCTGATATCGAATCAAAAAAAGATGCGCTCACACCACTGCTACTTGT 720
QY 721 ATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTAAT 780
Dd 721 ATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTAAT 780
QY 781 CGCTCGATAGATATGGAAGAACTGCTCTCATCTTGTGATGTTGGATCAGCAAGT 840
Dd 781 CGCTCGATAGATATGGAAGAACTGCTCTCATCTTGTGATGTTGGATCAGCAAGT 840
QY 841 ATAGTCAGCCCTTACTTGGAGCAAAATGTTGATGATCTTCTCAAGATCTGGAAGCGG 900
Dd 841 ATAGTCAGCCCTTACTTGGAGCAAAATGTTGATGATCTTCTCAAGATCTGGAAGCGG 900
QY 901 CCAGAGATATGCTGTTTCTTAGTCATCATCATG 933
Dd 901 CCAGAGATATGCTGTTTCTTAGTCATCATCATG 933
```

RESULT 2

ADC15396
ID ADC15396 standard; DNA; 939 BP.

XX AC
XX ADC15396;

DT 18-DEC-2003 (first entry)

XX Human breast tumour protein DNA, SEQ ID 344.

DE Cytostatic; Gene therapy; breast cancer; breast tumour protein; human;
XX ds.

OS Homo sapiens.

XX WO2003013431-A2.

XX 20-FEB-2003.

XX 05-AUG-2002; 2002WO-US024917.

XX 07-AUG-2001; 2001US-00924400.

XX 20-FEB-2002; 2002US-00079137.

XX 02-AUG-2002; 2002US-00212679.

XX (CORI-) CORIXA CORP.

XX Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;
XX Kaios MD;

XX WPI; 2003-342398/32.

XX New polynucleotide, useful for preparing a composition for diagnosing,
XX treating or preventing cancer.

XX Claim 1; SEQ ID NO 344; 308pp; English.

XX The present invention relates to compositions and methods for the therapy
CC and diagnosis of cancer, particularly breast cancer. The method for
CC detecting the presence of a cancer in a patient comprises: obtaining a
CC biological sample from the patient; contacting the biological sample with
CC a binding agent that binds to the polypeptide; detecting in the sample an
CC amount of the polypeptide that binds to the binding agent; and comparing
CC the amount of the polypeptide to a predetermined cut-off value. Treating
CC breast cancer comprises administering a composition comprising breast
CC tumour proteins and nucleic acids, which simulates and/or expands T cells
CC specific for the tumour protein. The present sequence was used to
CC illustrate the invention.

XX SQ Sequence 939 BP; 273 A; 204 C; 249 G; 213 T; 0 U; 0 Other;

Query Match 97.9%; Score 913.8; DB 9; Length 939;
Best Local Similarity 99.1%; Pred. No. 3.6e-263;

Matches 931; Conservative 0; Mismatches 2; Indels 6; Gaps 1;

QY 1 ATGGTGGTTGAGTTGATTCATGCGCGGTGCTCTTCTGTGAAGAGCCATTGGTCTC 60

Dd 1 ATGGTGGTTGAGTTGATTCATGCGCGGTGCTCTTCTGTGAAGAGCCATTGGTCTC 60

QY 61 AGGAGCAAGATGGCGCAAGTGGTCTCTTCCCTGCTGAGGGGAGCGGCAAG 114

Dd 61 AGGAGCAAGATGGCGCAAGTGGTCTCTTCCCTGCTGAGGGGAGCGGCAAG 120

QY 115 AGCAACCTGGGCACTTCTGGAGACCAACAGCTCTCTGTGAAGCGCTTGGAGCAAG 174

Dd 121 AGCAACCTGGGCACTTCTGGAGACCAACAGCTCTCTGTGAAGCGCTTGGAGCAAG 180

QY 175 AGGTGCAAGTGGTCTGCCACTGCTTCCCTGCTGAGGGGAGCGGCAAGCAAGT 234

Dd 181 AGGTGCAAGTGGTCTGCCACTGCTTCCCTGCTGAGGGGAGCGGCAAGCAAGT 240

QY 235 GGCGCTTGGGAGACTACGATGACAGCGCTTCTATGATCCAGGTACCACTCCATGGA 294

Db	241	GTGCGTCTGGGGAGACTACGATGACAGCGCCCTTCTATGGATCCACAGTACCACTGTCATGGA	300
Qy	295	GAAGATCTGGACAAGCTCCACAGAGCTCCCTGGTGGGTAAAGTCCCCAGAAAAGGATCTC	354
Db	301	GAAGATCTGGACAAGCTCCAAGAGCTCCCTGGTGGGTAAAGTCCCCAGAAAGATCTC	360
Qy	355	ATCGTCATGCTCAGGGACACTGATGTGAACAAAGAGGGACAAGCAAAGAGGACTGCTCTTA	414
Db	361	ATCGTCATGCTCAGGGACAAGGATGTGAACAAAGAGGGACAAGCAAAGAGGACTGCTCTTA	420
Qy	415	CATCTGGCCCTCTGCCAATGGGAATTCAGAACTAGTAAAACTCTCGTGTGGACAGACCATCT	474
Db	421	CATCTGGCCCTCTGCCAATGGGAAATTCAGAACTAGTAAAACTCTCGTGTGGACAGACCATCT	480
Qy	475	CAACTTAATGTCTCTTGACAACAAAGAGGACACGCTCTGAACAAAGCCCGTACAAATCCACAG	534
Db	481	CAACTTAATGTCTCTTGACAACAAAGAGGACACGCTCTGAACAAAGCCCGTACAAATCCACAG	540
Qy	535	GAAGATGAATGTGCGGTTAATCTTGCTGGAACATGGCACTGATCCAAATATTCAGATGAG	594
Db	541	GAAGATGAATGTGCGGTTAATCTTGCTGGAACATGGCACTGATCCAAATATTCAGATGAG	600
Qy	595	TATGGAATPACCACTCTACACTATGCTCTCTPACAAATGAAGATAAAATTAATGGCCAAAGCA	654
Db	601	TATGGAATPACCACTCTACACTATGCTCTCTPACAAATGAAGATAAAATTAATGGCCAAAGCA	660
Qy	655	CTGCTCTTATACGGTCTGATATCGAATCAAAAACAAAGCATGGCTCTCACACCTGCTTA	714
Db	661	CTGCTCTTATACGGTCTGATATCGAATCAAAAACAAAGCATGGCTCTCACACCTGCTTA	720
Qy	715	CTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAAGCGGAAT	774
Db	721	CTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAAGCGGAAT	780
Qy	775	TTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATACTCTGTATGTTGTGGATCA	834
Db	781	TTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATACTCTGTATGTTGTGGATCA	840
Qy	835	GCAAGTATAGTCAGCCCTCTACTTGGACAAATGTTGATGTATCTTCTCAAGATCTGGAA	894
Db	841	GCAAGTATAGTCAGCCCTCTACTTGGACAAATGTTGATGTATCTTCTCAAGATCTGGAA	900
Qy	895	AGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG	933
Db	901	AGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG	939
RESULT 3			
ABT43733			
XX ID ABT43733 standard; cdNA; 1689 BP.			
XX AC ABT43733;			
XX DT			
XX DE 16-OCT-2003 (first entry)			
XX DT			
XX DE Molecule for disease detection and treatment (MDPT)-41 cdNA sequence.			
XX XX			
XX KW Human; Molecules for Disease Detection and Treatment; MDPT;			
XX KW MDDT-antagonist; MDDT-agonist; gene therapy; cardiant; cytosstatic;			
XX KW neuroprotective; cardiovascular disorder; neurological disorder;			
XX KW cell proliferative disorder; autoimmune disorder; inflammatory disorder;			
XX KW developmental disorder; cancer; steroid metabolic response; gene; ss.			
XX OS Homo sapiens.			
XX OS			
XX XX WO2003052049-A2.			
XX PN			
XX PD 26-JUN-2003.			
XX XX			
XX PF 09-JUL-2002; 2002WO-US021767.			
XX PR 09-JUL-2001; 2001US-0304298P.			

13-JUL-2001; 2001US-0305324P.
19-JUL-2001; 2001US-0307003P.
27-JUL-2001; 2001US-0308185P.
3-AUG-2001; 2001US-0310096P.
10-AUG-2001; 2001US-0311551P.
08-MAR-2002; 2002US-0363649P.
(INCY-) INCYTE GENOMICS INC.
Thornton M, Au-Young JK, Azimzai Y, Bandman O, Barroso I; Baughn MR, Becha SD, Borowsky ML, Ding L, Duggan BM, Elliott VS; Euerling BM, Forsythe IJ, Gandhi AR, Gletzen KJ, Gorvad AE; Griffin JA, Gururajan K, Haralia AJA, Ring HZ, Ison CH, Jones KA; Lal PG, Lee EA, Lee S, Li JX, Lu DAM, Marquis JP, Lehr-Mason FM; Chawla NK, Arvizu CS, Sanjanwala B, Sornasse T, Swarnakar A; Tang YT, Thangavelu K, Tran B, Tran UK, Warren BA, Xu Y, Yao MG; Yue H, Yue H, Zebardjian Y, Chang H;
WPI; 2003-533003/50.
P-PSDB; ABJ39131.
New Molecules for Disease Detection and Treatment polypeptides, useful for preparing a composition for diagnosing or treating e.g. cardiovascular or neurological disorders.
Claim 5; Page 276; 289pp; English.
This invention relates to novel polypeptides associated with Molecules for Disease Detection and Treatment (MDDT) and the cDNA sequences which encode them. MDDT-antagonists, MDDT-agonists or gene therapy may produce cardiac, cytostatic and neuroprotective activities. The polypeptides and cDNA sequences of the invention may be useful for the preparation of a composition for the diagnosis or treatment of a disease which is associated with decreased expression or over-expression of functional MDDT proteins, for example cardiovascular, neurological, cell proliferative, autoimmune/inflammatory or developmental disorders. They may also be useful in the treatment and diagnosis of cancer, diseases treated with steroids and disorders caused by the metabolic response to treatment with steroids. The present sequence is the cDNA sequence encoding a human Molecule for Disease Detection and Treatment (MDDT) of the invention
Sequence 1689 BP; 499 A; 360 C; 431 G; 399 T; 0 U; 0 Other;
Query Match 92.6%; Score 864.2; DB 8; Length 1689;
Best Local Similarity 98.6%; Pred. No. 3.8e-248;
Matches 926; Conservative 0; Mismatches 3; Indels 10; Gaps 5;
Qy 1 ATGGTGGTTGAGTTGATTCATTCAGTCCGGCTGCTCTTCTGTGAAGAGCCATTGGTCTC 60
Db 28 ATGGTGGCTGAGTTGATTCAATTCGGCGCTGCTCTTCTGTGAAGAGCCATTGGTCTC 87
Qy 61 AGGAGCAAGATGGCGAAGTGGTG-----CTGCTTTCCCTGCTGCAGGGGAGCGGCAAG 114
Db 88 AGAGCAAGATGGCGAAGTGGTGCTGCTCCACTGTTTCCCTGCTGCAGGGGAGCGGCAAG 147
Qy 115 AGCAAGTGGGCACTTCTGGAGACCAACAGACTCTCTGTGAAGAGCGTTGGGAGCAAG 174
Db 148 AGCAAGTGGGCACTTCTGGAGACCAACAGACTCTCTGTGAAGAGCGTTGGGAGCAAG 207
Qy 175 AGTGCAAGTGGTGTGCGCACTGCTTCCCTGCTGCAGGGGAGCGGCAAGCAAGCTG 234
Db 208 AGTGCAAGTGGTGTGCGCACTGCTTCCCTGCTGCAGGGGAGCGGCAAGCAAGCTG 267
Qy 235 GCGCGTTGGGAGACTACCATGACAGCGCCTTCATGGATCCCAAGTACCAGTCCATGGA 294
Db 268 GTCGCTTGGGAGACTACCATGACAGCGCCTTCATGGATCCCAAGTACCAGTCCATGGA 327
Qy 295 GAGATCTGGAAGAAGCTCCACAGAGTGCCTGTGGGTAAAGTCCCCAGAAAGGATCTC 354
Db 328 GAGATCTGGAAGAAGTCCACAGAGTGCCTGTGGGTAAAGTCCCCAGAAAGGATCTC 387
Qy 355 ATCGTCAATGCTCAGGACACTGATGTGAACAGAGGGAACAAGCAAGAGCACTGCTCTA 414

Db 388 ATCGTCATGCTCAGGACACGATGTGAACAAGAGGACAAAGAGAGACTGCTCTA 447
Qy 415 CATCTGGCTCTGCCAATGGGAATTCAGAAAGTAGTAATAACTCGTCTGGACAGAGATGT 474
Db 448 CATCTGGCTCTGCCAATGGGAATTCAGAAAGTAGTAATAACTCGTCTGGACAGAGATGT 507
Qy 475 CAACTTAATGTCTCTGACAAACAAAGAGAGACAGCTCTTGACAAAGCCGCTACAATGCCAG 534
Db 508 CAACTTAATGTCTCTGACAAACAAAGAGAGACAGCTCTTGACAAAGCCGCTACAATGCCAG 567
Qy 535 GAAGATGAATGCGTGAATGTGCTGGAACATGGCACTGATCCAAATATTCAGATGAG 594
Db 568 GAAGATGAATGCGTGAATGTGCTGGAACATGGCACTGATCCAAATATTCAGATGAG 627
Qy 595 TATGAAATACCACTCTACACTATGCTGTCTAATGAAGATAAATTAATGSCCAAAGCA 654
Db 628 TATGAAATACCACTCTACACTATGCTGTCTAATGAAGATAAATTAATGSCCAAAGCA 686
Qy 655 CTGCTCTTATACGCTCTGATATCGAATCAAAAACAGCATGGCTCACACACTGCTA 714
Db 687 CTGCTCTTATACGCTCTGATATCGAATCAAAAACAGCATGGCTCACACACTGCTA 745
Qy 715 CTGCTCTTATACGCTCTGATATCGAATCAAAAACAGCATGGCTCACACACTGCTA 774
Db 746 CTGCTCTTATACGCTCTGATATCGAATCAAAAACAGCATGGCTCACACACTGCTA 803
Qy 775 TTAATGCGCTGATATGGAAGAACTGCTCTCATACCTGCTGTATGTTGTGATCA 834
Db 804 TTAATGCGCTGATATGGAAGAACTGCTCTCATACCTGCTGTATGTTGTGATCA 863
Qy 835 GCAAGTATAGTACGCTCTGATATGGAAGAACTGCTCTCATACCTGCTGTATGTTGTGATCA 894
Db 864 GCAAGTATAGTACGCTCTGATATGGAAGAACTGCTCTCATACCTGCTGTATGTTGTGATCA 923
Qy 895 AGACGGCCAGAGATGATGCTGTTCTTCTAGTCATCATG 933
Db 924 AGACGGCCAGAGATGATGCTGTTCTTCTAGTCATCATG 962

RESULT 4
ADCL15394
ID ADC15394 standard; DNA; 876 BP.
XX AC ADCL15394;
XX AC ADCL15394;
XX AC ADCL15394;
DT 18-DEC-2003 (first entry)
DE Human breast tumour protein DNA, SEQ ID 342.
XX Cystostatic; Gene therapy; breast cancer; breast tumour protein; human;
XX ds.
XX Homo sapiens.
OS
XX WO2003013431-A2.
XX 20-FEB-2003.
PD
XX 05-AUG-2002; 2002WO-US024917.
PF
XX 07-AUG-2001; 2001US-00924400.
PR 20-FEB-2002; 2002US-00079137.
PR 02-AUG-2002; 2002US-00212679.
XX
XX (CORI-) CORIXA CORP.
XX Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;
PI Kalos MD;
XX
XX WPI; 2003-342398/32.
XX
XX New polynucleotide, useful for preparing a composition for diagnosing,
PT

PT treating or preventing cancer.
XX Claim 1; SEQ ID NO 342; 308pp; English.
XX
CC The present invention relates to compositions and methods for the therapy
CC and diagnosis of cancer, particularly breast cancer. The method for
CC detecting the presence of a cancer in a patient comprises: obtaining a
CC biological sample from the patient; contacting the biological sample with
CC a binding agent that binds to the polypeptide; detecting in the sample an
CC amount of the polypeptide that binds to the binding agent; and comparing
CC the amount of the polypeptide to a predetermined cut-off value. Treating
CC breast cancer comprises administering a composition comprising breast
CC tumour proteins and nucleic acids, which simulates and/or expands T cells
CC specific for the tumour protein. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 876 BP; 261 A; 193 C; 222 G; 200 T; 0 U; 0 Other;
Query Match 89.5%; Score 835; DB 9; Length 876;
Best Local Similarity 100.0%; Pred. No. 1.5e-239;
Matches 835; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 99 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCAACAGCTCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCAACAGCTCTCTGTGAA 101
Qy 159 GACGCTTGGGAGCAAGAGGTGCAAGTGGTCTGCCCTCTCCCTGTCGAGGGGAG 218
Db 102 GACGCTTGGGAGCAAGAGGTGCAAGTGGTCTGCCCTCTCCCTGTCGAGGGGAG 161
Qy 219 CGGCAAGAGCAACGTGGGCGCTTGGGAGACTAGCATGACAGCGCTTCATGATCCAG 278
Db 162 CGGCAAGAGCAACGTGGGCGCTTGGGAGACTAGCATGACAGCGCTTCATGATCCAG 221
Qy 279 GTACACGCTCCATGGAGAAGATCTGGACAGCTCCACAGAGCTGCTGGTGGGTAAGT 338
Db 222 GTACACGCTCCATGGAGAAGATCTGGACAGCTCCACAGAGCTGCTGGTGGGTAAGT 281
Qy 339 CCCAGAGAAAGATCTCATCTGCTCATGCTCAGGACACTGATGTGAACAAGAGGCAAGCA 398
Db 282 CCCAGAGAAAGATCTCATCTGCTCATGCTCAGGACACTGATGTGAACAAGAGGCAAGCA 341
Qy 399 AAAGAGAGCTCTCTACATCTGGCTCTGCCAATGGGAATTCAGAACTAGTAACCTG 458
Db 342 AAAGAGAGCTCTCTACATCTGGCTCTGCCAATGGGAATTCAGAACTAGTAACCTG 401
Qy 459 GCTGGACAGAGATGTCAACTTAATGTCTTGAACAACAAAGAGGACAGCTCTGACAAA 518
Db 402 GCTGGACAGAGATGTCAACTTAATGTCTTGAACAACAAAGAGGACAGCTCTGACAAA 461
Qy 519 GGGCGTCAATGCGGAGAGATGAATGTGCTTAAATGTGCTGGAACATGCGACTGATCC 578
Db 462 GGGCGTCAATGCGGAGAGATGAATGTGCTTAAATGTGCTGGAACATGCGACTGATCC 521
Qy 579 AAATATTCAGATGATGGAATACCACTCTACACTATGCTCTACATGAAGATAA 638
Db 522 AAATATTCAGATGATGGAATACCACTCTACACTATGCTCTACATGAAGATAA 581
Qy 639 ATTAATGCCAAAGCACTGCTCTTATACGGTCTGATATCGAATCAAAAACAGCATGG 698
Db 582 ATTAATGCCAAAGCACTGCTCTTATACGGTCTGATATCGAATCAAAAACAGCATGG 641
Qy 699 CCTCACACCACTGCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 758
Db 642 CCTCACACCACTGCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 701
Qy 759 CAAGAAAAAGCAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC 818
Db 702 CAAGAAAAAGCAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC 761
Qy 819 TGTATGTTGTGATCAGCAAGTATAGTACGCTCTTACTGAGCAAAATGTTGATGATC 878
Db 762 TGTATGTTGTGATCAGCAAGTATAGTACGCTCTTACTGAGCAAAATGTTGATGATC 821

879 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG 933
822 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG 876

RESULT 5
ADCL5393
ID ID ADCL5393 standard; DNA; 876 BP.
AC AC ADCL5393;
DT 18-DEC-2003 (first entry)
XX Human breast tumour protein DNA, SEQ ID 341.
DE Cytostatic; Gene therapy; breast cancer; breast tumour protein; human;
KW ds.
XX Homo sapiens.
OS WO2003013431-A2.
PN 20-FEB-2003.
XX 05-AUG-2002; 2002WO-US024917.
PF 07-AUG-2001; 2001US-00924400.
PR 20-FEB-2002; 2002US-00079137.
PR 02-AUG-2002; 2002US-00212679.
XX (CORI-) CORIXA CORP.
PA Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;
XX Kalos MD;
PI WPI; 2003-342398/32.
XX New polynucleotide, useful for preparing a composition for diagnosing,
PT treating or preventing cancer.
XX Claim 1; SEQ ID NO 341; 308pp; English.

The present invention relates to compositions and methods for the therapy
and diagnosis of cancer, particularly breast cancer. The method for
detecting the presence of a cancer in a patient comprises: obtaining a
biological sample from the patient; contacting the biological sample with
a binding agent that binds to the polypeptide; detecting in the sample an
amount of the polypeptide that binds to the binding agent; and comparing
the amount of the polypeptide to a predetermined cut-off value. Treating
breast cancer comprises administering a composition comprising breast
tumour proteins and nucleic acids, which simulates and/or expands T cells
specific for the tumour protein. The present sequence was used to
illustrate the invention.

Sequence 876 BP; 261 A; 193 C; 222 G; 200 T; 0 U; 0 Other;
Query Match 89.2%; Score 831.8; DB 9; Length 876;
Best Local Similarity 99.8%; Pred. No. 1.4e-238;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

99 CAGGGGAGCGGCAAGAGCAACGTTGGGCACTTCTGGAGACCAACGACTCTCTGTGAA 158
42 CAGGGGAGCGGCAAGAGCAACGTTGGGCACTTCTGGAGACCAACGACTCTCTGTGAA 101
159 GACGCTTGGGAGCAGAGTCAAGTGTGCTGCCACTGTTCCCTGCTGCAGGGGGAG 218
102 GACGCTTGGGAGCAGAGTCAAGTGTGCTGCCACTGTTCCCTGCTGCAGGGGGAG 161
219 CGGCAAGAGCAACGTTGGGCGCTTGGGAGACTACGATGACAGCGCTTCATGGATCCAG 278
162 CGGCAAGAGCAACGTTGGGCGCTTGGGAGACTACGATGACAGCGCTTCATGGATCCAG 221

QY 279 GTACACGCTCCATGAGGAAGATCTGGACAAGACTCCACAGAGCTGCTGGTGGGTAAAGT 338
DB 222 GTACACGCTCCATGAGGAAGATCTGGACAAGACTCCACAGAGCTGCTGGTGGGTAAAGT 281
QY 339 CCCAGAAAAGGATCTCATGCTCAGGCACTGATGTGAACAAGAGGGGACAAGCA 398
DB 282 CCCAGAAAAGGATCTCATGCTCAGGCACTGATGTGAACAAGAGGGGACAAGCA 341
QY 399 AAAGAGGACTGCTCTACATCTGGGCTCTGCCAATGGGAATTCAGAACTAGTAAACTG 458
DB 342 AAAGAGGACTGCTCTACATCTGGGCTCTGCCAATGGGAATTCAGAACTAGTAAACTG 401
QY 459 GCTGACACAGAGATGTCACACTTAAATGCTTGAACAACAAAAGAGGACAGCTCTGACAAA 518
DB 402 GCTGACACAGAGATGTCACACTTAAATGCTTGAACAACAAAAGAGGACAGCTCTGACAAA 461
QY 519 GGCCTTACAATGCCAGGAGATGAATGTCGTTAATGTTGTGGAACATGGCAGCTGATCC 578
DB 462 GGCCTTACAATGCCAGGAGATGAATGTCGTTAATGTTGTGGAACATGGCAGCTGATCC 521
QY 579 AAATATTCAGATGATGGAATACCACTACACTATGCTCTACAAATGAAGATAA 638
DB 522 AAATATTCAGATGATGGAATACCACTACACTATGCTCTACAAATGAAGATAA 581
QY 639 ATTAATGCCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 698
DB 582 ATTAATGCCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 641
QY 699 CCTCACACACTGCTACTGTTGTATACATGACAAAACAGCAAGTGGTCAAAATTTTAAAT 758
DB 642 CCTCACACACTGCTACTGTTGTATACATGACAAAACAGCAAGTGGTCAAAATTTTAAAT 701
QY 759 CAAGAAAAAAGCGAATTTAAATGCGCTGATATGGAAGAACTGCTCTCATACTTGC 818
DB 702 CAAGAAAAAAGCGAATTTAAATGCGCTGATATGGAAGAACTGCTCTCATACTTGC 761
QY 819 TGTATGTTGTGATCAGCAAGTATAGTCAGGCTTACTTACTGAGCAAAATGTTGATGATC 878
DB 762 TGTATGTTGTGATCAGCAAGTATAGTCAGGCTTACTTACTGAGCAAAATGTTGATGATC 821
QY 879 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933
DB 822 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 876

RESULT 6
AAC81016
ID AAC81016 standard; cDNA; 879 BP.
XX AAC81016;
AC AAC81016;
XX 13-FEB-2001 (first entry)
DE Human breast tumour-specific antigen cDNA SEQ ID NO: 314.
XX Human; breast tumour-specific antigen; cytostatic; vaccine;
KW breast cancer; B18Ag1; B11Ag1; B15Ag1; B8;
OS Homo sapiens.
XX WO200061753-A2.
XX 19-OCT-2000.
XX 07-APR-2000; 2000WO-US009312.
XX 09-APR-1999; 99US-00289198.
PR 28-OCT-1999; 99US-00429755.
PR 23-MAR-2000; 2000US-00534825.
XX (CORI-) CORIXA CORP.
PA Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
PI

[illegible]

Db 42 CAGGGGAGCGGCAAGAGCAACCGTGGCACTTCTTGAGACCAACAGCACTCTCTGTGAA 101
QY 159 GACGCTTTGGGAGCAAGAGGTGCAAGTGTCTGCTGCCACTGTTCCCTCTGCTGACGGGGAG 218
Db 102 GACGCTTTGGGAGCAAGAGGTGCAAGTGTCTGCTGCCACTGTTCCCTCTGCTGACGGGGAG 151
QY 219 CGGCAAGAGCAACGTTGGGCGCTTTGGGAGACTACGATGACAGCGCTTTCATGATCCAG 278
Db 162 CGGCAAGAGCAACGTTGGGCGCTTTGGGAGACTACGATGACAGCGCTTTCATGATCCAG 221
QY 279 GTACCAAGTCTCATGAGAGAGTCTGGAAGTCTGGAAGTCTGGAAGTCTGGAAGTCTGGAAGT 338
Db 222 GTACCAAGTCTCATGAGAGAGTCTGGAAGTCTGGAAGTCTGGAAGTCTGGAAGTCTGGAAGT 281
QY 339 CCCAGAGAGAGTCTCATGATGCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 398
Db 282 CCCAGAGAGAGTCTCATGATGCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 341
QY 399 AAGAGGACTGCTCTACATCTGCGCTCTGCAATGGGAATTCAGAGTCTGAGAGTCTGAGAGT 458
Db 342 AAGAGGACTGCTCTACATCTGCGCTCTGCAATGGGAATTCAGAGTCTGAGAGTCTGAGAGT 401
QY 459 GCTGGAAGAGTCTCAACTTAATGTCCTTGAACAAAGAGAGGAGAGTCTGACAAA 518
Db 402 GCTGGAAGAGTCTCAACTTAATGTCCTTGAACAAAGAGAGGAGAGTCTGACAAA 461
QY 519 GCGCGTCAATGCGAGAGAGTGAATGCGTTAATGTTGCTGGAACATGCACTGATCC 578
Db 462 GCGCGTCAATGCGAGAGAGTGAATGCGTTAATGTTGCTGGAACATGCACTGATCC 521
QY 579 AAATATTCAGATGAGTGAATGCAATGCACTGATGCTGCTGCAATGAGATAA 638
Db 522 AAATATTCAGATGAGTGAATGCAATGCACTGATGCTGCTGCAATGAGATAA 581
QY 639 ATTAATGCCAAAGCACTGCTTTATAGTGTGCTGATGATGAAATCAAAAACAGCATGG 698
Db 582 ATTAATGCCAAAGCACTGCTTTATAGTGTGCTGATGATGAAATCAAAAACAGCATGG 641
QY 699 CTTACACCACTGCTTACTGTTATACATGACAAACAGCAAGTGTGAAATTTTAAAT 758
Db 642 CTTACACCACTGCTTACTGTTATACATGACAAACAGCAAGTGTGAAATTTTAAAT 701
QY 759 CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATGGAAGAACTGCTCTCATATGTC 818
Db 702 CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATGGAAGAACTGCTCTCATATGTC 761
QY 819 TGTATGTTGTGGATCAGCAAGTATAGTACGCTTACTTGGCAAAATGTTGATGATC 878
Db 762 TGTATGTTGTGGATCAGCAAGTATAGTACGCTTACTTGGCAAAATGTTGATGATC 821
QY 879 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCAATCATG 933
Db 822 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCAATCATG 876

RESULT 8
AAS63919
ID AAS63919 standard; cdna; 879 BP.
XX
AC AAS63919;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human prostate cdna clone B305D splice variant #11 open reading frame.
XX
KW Human; prostate cancer; ss; cytosatic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN W0200173032-A2.
XX
PD 04-OCT-2001.
XX

PF 27-MAR-2001; 2001WO-US009919.
XX
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Ratter MW, Stolk JA, Day CH, Vedwick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2001-539232/73.
DR P-PSDB; AAU69821.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
XX the diagnosis and treatment of cancer, especially prostate cancer.
XX
XX Claim 1; Page 408; 579pp; English.
XX
XX The invention relates to isolated prostate-specific polynucleotides,
XX polypeptides, fusion proteins of the polypeptides, antibodies raised
XX against the polypeptides (or antigenic epitopes derived from them) and
XX antigen-presenting cells expressing the polypeptides. The antibodies are
XX useful for detecting the presence of cancer, especially prostate cancer.
XX The polypeptides, polynucleotides and the antigen-presenting cells are
XX useful for stimulating and/or expanding T cells specific for a tumour
XX protein, and for inhibiting the development of cancer especially prostate
XX cancer. Compositions comprising the polynucleotide and/or polypeptide are
XX useful for stimulating an immune response, and for treating cancer. The
XX oligonucleotide is useful for detecting cancer. The present sequence is a
XX prostate specific polynucleotide of the invention
XX
XX Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;
XX
XX Query Match 89.2%; Score 831.8; DB 4; Length 879;
XX Best Local Similarity 99.8%; Pred. No. 1.4e-238;
XX Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 99 CAGGGGAGCGGCAAGAGCAACCGTGGCACTTCTTGAGACCAACAGCACTCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGAGCAACCGTGGCACTTCTTGAGACCAACAGCACTCTCTGTGAA 101
QY 159 GACGCTTTGGGAGCAAGAGGTGCAAGTGTGCTGCCACTGTTCCCTCTGCTGAGGGAG 218
Db 102 GACGCTTTGGGAGCAAGAGGTGCAAGTGTGCTGCCACTGTTCCCTCTGCTGAGGGAG 161
QY 219 CGGCAAGAGCAACGTTGGGCGCTTTGGGAGACTACGATGACAGCGCTTTCATGATCCAG 278
Db 162 CGGCAAGAGCAACGTTGGGCGCTTTGGGAGACTACGATGACAGCGCTTTCATGATCCAG 221
QY 279 GTACCAAGTCTCATGAGAGAGTCTGGAAGTCTGGAAGTCTGGAAGTCTGGAAGTCTGGAAGT 338
Db 222 GTACCAAGTCTCATGAGAGAGTCTGGAAGTCTGGAAGTCTGGAAGTCTGGAAGTCTGGAAGT 281
QY 339 CCCAGAGAGAGTCTCATGATGCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 398
Db 282 CCCAGAGAGAGTCTCATGATGCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 341
QY 399 AAGAGGACTGCTCTACATCTGCGCTCTGCAATGGGAATTCAGAGTCTGAGAGTCTGAGAGT 458
Db 342 AAGAGGACTGCTCTACATCTGCGCTCTGCAATGGGAATTCAGAGTCTGAGAGTCTGAGAGT 401
QY 459 GCTGGAAGAGTCTCAACTTAATGTCCTTGAACAAAGAGAGGAGAGTCTGACAAA 518

ACA59727
ID ACA59727 standard; cDNA; 879 BP.
XX AC
XX ACA59727;
XX 10-JUN-2003 (first entry)
XX Prostate cancer therapy associated cDNA #464.
DE
XX Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW immunogen; cancer; prostate specific antigen; PSA;
KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW PSMA; gene; ss.
XX Homo sapiens.
XX US2002192763-A1.
XX 19-DEC-2002.
XX 29-JUN-2001; 2001US-00895793.
XX 04-OCT-1999; 99US-01574559.
XX 04-OCT-2000; 2000US-00679272.
XX 28-MAR-2001; 2001US-00822827.
XX (XUJI/) XU J.
XX (DILL/) DILLON D C.
XX (MITC/) MITCHAM J L.
XX (HARL/) HARLOCKER S L.
XX (JIAN/) JIANG Y.
XX (KALO/) KALOS M D.
XX (FANG/) FANGER G R.
XX (RETT/) RETTER M W.
XX (STOL/) STOLK J A.
XX (DAYC/) DAY C H.
XX (VEDV/) VEDVICK T S.
XX (CART/) CARTER D.
XX (LISX/) LI S X.
XX (WANG/) WANG A.
XX (SKEI/) SKEIKY Y A W.
XX (HEPL/) HEPLER W T.
XX (HEND/) HENDERSON R A.
XX (HURA/) HURAL J.
XX (MCNE/) MCNEILL P D.
XX (HOUG/) HOUGHTON R L.
XX (DBAS/) Y DE BASSOLS C V.
XX (FOYT/) FOY T M.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
PI McNeill PD, Houghton RL, Y De BassolsCV, Foy TM;
XX WPI; 2001-245062/25.
XX Prostate specific protein and its encoding polynucleotide, useful for the
PT treatment and diagnosis of prostate cancer.
XX Example 11; SEQ ID NO 531; 85pp; English.
XX The invention describes a fusion protein comprising at least one amino
CC acid sequence of immunogenic portions of any of the 3 sequences not
CC defined in the specification, or sequences having at least 70 or 90 %
CC sequence identity to any one of the 3 sequences defined in the USPTO web
CC site, which is encoded by any of the 4 nucleotide sequences not defined
CC in the specification. The fusion protein, composition and methods are
CC useful for diagnosing, preventing and/or treating cancer, particularly
CC prostate cancer. The proteins are useful as markers to indicate the
CC presence or absence of cancer. This sequence represents a prostate cancer
CC therapy associated cDNA. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from the US patent office at

CC seqdata.uspto.gov/sequence.html?DocID=US20020192763
XX
SQ Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;
Query Match 89.2%; Score 831.8; DB 5; Length 879;
Best Local Similarity 99.8%; Pred. No. 1.4e-338;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 99 CAGGGGAGCGGCAAGAGCAACGCTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA 158
Db
42 CAGGGGAGCGGCAAGAGCAACGCTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA 101
QY 159 GAGCTTTGGAGCAAGAGGTGCAAGTGGTCTGCCACTGCTTCCCTGCTGCAAGGGGGAG 218
Db
102 GAGCTTTGGAGCAAGAGGTGCAAGTGGTCTGCCACTGCTTCCCTGCTGCAAGGGGGAG 161
QY 219 CGGCAAGAGCAACGCTGGGCGCTTTGGGAGACTACGATGACAGCGCCTTTCATGATCCAG 278
Db
162 CGGCAAGAGCAACGCTGGGCGCTTTGGGAGACTACGATGACAGCGCCTTTCATGATCCAG 221
QY 279 GTACCACTCCATGGAGAAAGATCTGACAAAGCTCCACAGAGCTGCTGTGGGGTAAAGT 338
Db
222 GTACCACTCCATGGAGAAAGATCTGACAAAGCTCCACAGAGCTGCTGTGGGGTAAAGT 281
QY 339 CCCAGAAAGGATCTCATGCTCATGCTCAGGGACATGTGATGCAACAAAGAGGACACGCA 398
Db
282 CCCAGAAAGGATCTCATGCTCATGCTCAGGGACATGTGATGCAACAAAGAGGACACGCA 341
QY 399 AAAGAGGACTGCTTACATCTGCCCTCTGCAATGGGAATTCAGAGTAGTAAACCTCGT 458
Db
342 AAAGAGGACTGCTTACATCTGCCCTCTGCAATGGGAATTCAGAGTAGTAAACCTCGT 401
QY 459 GCTGGACAGACGATGTCACCTTAATGCTCTTGACACAAAGAGGACACGCTCGACAA 518
Db
402 GCTGGACAGACGATGTCACCTTAATGCTCTTGACACAAAGAGGACACGCTCGACAA 461
QY 519 GGCGGTACAAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAAACATGGCACTGATCC 578
Db
462 GGCGGTACAAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAAACATGGCACTGATCC 521
QY 579 AAATATTCAGATGAGTATGGAATACCACTCTACACTATGCTGTCTACAAATCAAGATA 638
Db
522 AAATATTCAGATGAGTATGGAATACCACTCTACACTATGCTGTCTACAAATCAAGATA 581
QY 639 ATTAATGGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAACCAAGCATGG 698
Db
582 ATTAATGGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAACCAAGCATGG 641
QY 699 CCTCACACCACTGCTACTTGGTATACATGAGCAAAACAGCAAGTGGTGAATTTTAAAT 758
Db
642 CCTCACACCACTGCTACTTGGTATACATGAGCAAAACAGCAAGTGGTGAATTTTAAAT 701
QY 759 CAAGAAAAAGCGAAATTTAAATCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC 818
Db
702 CAAGAAAAAGCGAAATTTAAATCGCTGGTATGATATGGAAGAACTGCTCTCATACTTGC 761
QY 819 TGATATGTTGGATCAAGCAAGTATAGTACGCTCTTACTTGAGCAAAATGTTGATGATC 878
Db
762 TGATATGTTGGATCAAGCAAGTATAGTACGCTCTTACTTGAGCAAAATGTTGATGATC 821
QY 879 TTCTCAGATCTGGAAGAGCGCCAGGAGTAGTGTGTTTCTTAGTCATCATCATG 933
Db
822 TTCTCAGATCTGGAAGAGCGCCAGGAGTAGTGTGTTTCTTAGTCATCATCATG 876
RESULT 11
ABL95290
ID ABL95290 standard; cDNA; 879 BP.
XX
XX ABL95290;
XX AC ABL95290;
XX 19-JUL-2002 (first entry)
XX

XX Homo sapiens.
 XX WO200190152-A2.
 XX 29-NOV-2001.
 XX 22-MAY-2001; 2001WO-US016776.
 XX 24-MAY-2000; 2000US-00577505.
 XX 08-JUN-2000; 2000US-00590583.
 XX 26-OCT-2000; 2000US-00699295.
 XX 16-MAR-2001; 2001US-00810936.
 XX (CORI-) CORIXA CORP.
 XX Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
 XX Wang A, Skeiky YAW, Harlocker SL, Day CH;
 XX WPI; 2002-089919/12.
 XX P-PSDB; AAU74385.
 XX New breast tumor proteins and polynucleotides encoding them, useful for
 XX treating and/or preventing cancer, particularly breast cancer, and for
 XX eliciting humoral and/or cellular immune response.
 XX Claim 1; Page 231-232; 245pp; English.
 XX The invention relates to novel breast tumour polynucleotides and
 XX polypeptides. The polypeptides and polynucleotides are useful in
 XX pharmaceutical compositions for treating and/or preventing cancer,
 XX particularly breast cancer, and for eliciting an immune response,
 XX may be used as probes or primers for nucleic acid hybridisation, in the
 XX design and preparation of ribozyme molecules for inhibiting expression of
 XX tumour polypeptides and proteins, and in recombinant DNA molecules to
 XX direct expression of a polypeptide in host cells. AAS99570-AAS9988
 XX represent novel human breast cancer protein coding sequences and PCR
 XX primers of the invention
 XX
 XX Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;
 XX
 XX Query Match 89.2%; Score 831.8; DB 6; Length 879;
 XX Best Local Similarity 99.8%; Pred. No. 1.4e-238;
 XX Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX 99 CAGGGGAGCGGCAAGAGCAACGTGGGACCTTCTGGAGACCAACAGACTCTCTGTGAA 158
 XX 42 CAGGGGAGCGGCAAGAGCAACGTGGGACCTTCTGGAGACCAACAGACTCTCTGTGAA 101
 XX 159 GACGCTTGGGAGCAAGAGTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 218
 XX 102 GACGCTTGGGAGCAAGAGTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 161
 XX 219 CGGCAAGAGCAACGTGGGCGCTTGGGAGACTACGATGACAGCGCTTTCATGGATCCAG 278
 XX 162 CGGCAAGAGCAACGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 221
 XX 279 GTACACGCTCCATGGAGAGACTTGGCAAGCTTCCACAGAGCTGCTGGTGGGTTAAAGT 338
 XX 222 GTACACGCTCCATGGAGAGACTTGGCAAGCTTCCACAGAGCTGCTGGTGGGTTAAAGT 281
 XX 339 CCCGAGAAGGATCTCATCGTCTGAGGACACTGATGTGAACAAGAGGAGGACAGCA 398
 XX 282 CCCGAGAAGGATCTCATCGTCTGAGGACACTGATGTGAACAAGAGGAGGACAGCA 341
 XX 399 AAAGAGGACTGCTTACATCTGGGCTTGGCAATGGGAATTCAGAGTGTAAAGTTCGT 458
 XX 342 AAAGAGGACTGCTTACATCTGGGCTTGGCAATGGGAATTCAGAGTGTAAAGTTCGT 401
 XX 459 GCTGGACAGAGTGTCAACTATATGCTTGTGCAACAAGAGGAGGACGCTCTGCAAA 518
 XX 402 GCTGGACAGAGTGTCAACTATATGCTTGTGCAACAAGAGGAGGACGCTCTGCAAA 461

QY 519 GGCGGTACATGCCAGGAGATGATGCGTAAATGTTGCTGGAACTGGCACTGATCC 578
 DB 462 GGCGGTACATGCCAGGAGATGATGCGTAAATGTTGCTGGAACTGGCACTGATCC 521
 QY 579 AAATATTCAGATGATGGAATACCACTTACATCTGCTGCTCAATGAAGATAA 638
 DB 522 AAATATTCAGATGATGGAATACCACTTACATCTGCTGCTCAATGAAGATAA 581
 QY 639 ATTAATGGCCAAAGCACCTGCTTATACGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 698
 DB 582 ATTAATGGCCAAAGCACCTGCTTATACGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 641
 QY 699 CCTCACCACTGCTACTTGGTATACATGAGCAAAACAGCAAGTGGTGAATTTTAAAT 758
 DB 642 CCTCACCACTGCTACTTGGTATACATGAGCAAAACAGCAAGTGGTGAATTTTAAAT 701
 QY 759 CAAGAAAAAGCGAATTTAAATGCGCTGGATGATATGGAAGAACTGCTCTCATATCTGC 818
 DB 702 CAAGAAAAAGCGAATTTAAATGCGCTGGATGATATGGAAGAACTGCTCTCATATCTGC 761
 QY 819 TGTATGTTGTGGATCAGCAAGTATAGTCAAGCCCTCTTCTTGGCAAAATGTTGATGTATC 878
 DB 762 TGTATGTTGTGGATCAGCAAGTATAGTCAAGCCCTCTTCTTGGCAAAATGTTGATGTATC 821
 QY 879 TTCTCAAGATCTGGAAGACGCGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933
 DB 822 TTCTCAAGATCTGGAAGACGCGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 876

RESULT 13

ACC95454
 ID ACC95454 standard; cDNA; 879 BP.

XX AC ACC95454;
 XX DT 28-AUG-2003 (first entry)

XX DE Prostate tumour specific cDNA sequence SEQ ID 531.
 XX KW Cytostatic; gene therapy; prostate-specific protein; PSP; human;
 XX KW immune response; prostate cancer; ss.

XX OS Homo sapiens.
 XX PN WO200289747-A2.

XX PD 14-NOV-2002.
 XX PF 09-MAY-2002; 2002WO-US014753.

XX PR 09-MAY-2001; 2001US-00852911.
 XX PR 29-JUN-2001; 2001US-00895814.
 XX PR 10-DEC-2001; 2001US-00012896.

XX PA (CORI-) CORIXA CORP.
 XX PA Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
 XX PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
 XX PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
 XX PI McNeill PD, Houghton RL, Vinals Y De Bassolsc, Foy TM, Watanabe Y;
 XX PI Deng T;
 XX XX WPI; 2003-167130/16.

XX PT New prostate-specific proteins and genes, useful in gene therapy,
 XX PT particularly for stimulating an immune response in a patient, or treating
 XX PT prostate cancer in a patient, as well as for diagnosing prostate cancer
 XX PT in a patient.

XX PS Example 11; Page 475; 691pp; English.
 XX XX The present invention relates to novel prostate-specific proteins (PSP)

CC and their coding sequences. The PSPs and their coding sequences are
 CC useful for stimulating an immune response in a patient. Or for treating
 CC prostate cancer in a patient and for determining, detecting or diagnosing
 CC the presence of a cancer in a patient. The present sequence was used to
 CC illustrate the invention

XX
 SQ Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;
 Query Match 99.2%; Score 831.8; DB 7; Length 879;
 Best Local Similarity 99.8%; Pred. No. 1.4e-238;
 Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 99 CAGGGGAGCGGCAAGAGCAACCTGGGCACTTTGGAGACCAACAGCTCTCTGTGAA 158
 Db 42 CAGGGGAGCGGCAAGAGCAACCTGGGCACTTTGGAGACCAACAGCTCTCTGTGAA 101
 QY 159 GAGCTTTGGAGCAAGAGTGAAGTGGTCTGCCACTGCTCCCTGCTGCAGGGGGAG 218
 Db 102 GAGCTTTGGAGCAAGAGTGAAGTGGTCTGCCACTGCTCCCTGCTGCAGGGGGAG 161
 QY 219 CGGCAAGAGCAACCTGGGCGCTTTGGGGAGACTACGATGACAGCGCTTCCATGATCCCGAG 278
 Db 162 CGGCAAGAGCAACCTGGTCTGCTTTGGGGAGACTACGATGACAGCGCTTCCATGATCCCGAG 221
 QY 279 GTACCACTCCATGGAGAGATCTGGACAGCTCCACAGAGCTGCTGCTGGGGTAAAGT 338
 Db 222 GTACCACTCCATGGAGAGATCTGGACAGCTCCACAGAGCTGCTGCTGGGGTAAAGT 281
 QY 339 CCCAGAGAGGATCTCATCTGCTGCTCAGGACACTGTGTAACAAGAGGGACAGCA 398
 Db 282 CCCAGAGAGGATCTCATCTGCTGCTCAGGACACTGTGTAACAAGAGGGACAGCA 341
 QY 399 AAGAGAGCTGCTTACATCTGGCCCTGCGCAATGGGAATTCAGAGTAGTAAAGTCTGT 458
 Db 342 AAGAGAGCTGCTTACATCTGGCCCTGCGCAATGGGAATTCAGAGTAGTAAAGTCTGT 401
 QY 459 GCTGCAGACAGCTGCTCACTTAATGCTTGTGCAACAAAAAGAGGACAGCTCTGACAA 518
 Db 402 GCTGCAGACAGCTGCTCACTTAATGCTTGTGCAACAAAAAGAGGACAGCTCTGACAA 461
 QY 519 GCGCGTCAATGCCAGAGAGATGATGGTAAATGCTGCGAATGGCACTGGCACTATCC 578
 Db 462 GCGCGTCAATGCCAGAGAGATGATGGTAAATGCTGCGAATGGCACTGGCACTATCC 521
 QY 579 AAATATCCAGATGATGAAATACCACTTACACTATGCTGTGTACAAATCAAGATAA 638
 Db 522 AAATATCCAGATGATGAAATACCACTTACACTATGCTGTGTACAAATCAAGATAA 581
 QY 639 ATTAATGGCCAAAGCACTGCTTTATACGGTGTGATATCAATCAAAAAAAGCATGG 698
 Db 582 ATTAATGGCCAAAGCACTGCTTTATACGGTGTGATATCAATCAAAAAAAGCATGG 641
 QY 699 CTTCAACCACTGCTTGTGTATACATGAGCAAAACAGCAAGTGGTAAATTTTAAAT 758
 Db 642 CTTCAACCACTGCTTGTGTATACATGAGCAAAACAGCAAGTGGTAAATTTTAAAT 701
 QY 759 CAAGAAAAAGCGAATTTAAATGGCGTGGATAGATATGGAAGACTGCTCTCATCTGTC 818
 Db 702 CAAGAAAAAGCGAATTTAAATGGCGTGGATAGATATGGAAGACTGCTCTCATCTGTC 761
 QY 819 TGTATGTTGGATCAGCAAGTATAGTACAGCCCTTACTTGGCAAAATGTTGATGATC 878
 Db 762 TGTATGTTGGATCAGCAAGTATAGTACAGCCCTTACTTGGCAAAATGTTGATGATC 821
 QY 879 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933
 Db 822 TTCACAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 876

RESULT 14
 ADA11393

ID ADA11393 standard; cDNA; 879 BP.

XX

AC ADA11393;
 XX 06-NOV-2003 (first entry)
 DT Human breast cancer specific full length cDNA B305D-A ORF.
 XX ss; gene; human; breast cancer; cytostatic; tumour; gene therapy.
 XX Homo sapiens.
 OS US2002165371-A1.
 PN 07-NOV-2002.
 PD 07-AUG-2001; 2001US-00924400.
 PF 11-JAN-1996; 96US-00585392.
 PR 10-JAN-1997; 97WO-US000485.
 PR 09-APR-1997; 97US-00838762.
 PR 11-DEC-1997; 97US-00991789.
 PR 17-APR-1998; 98US-00062451.
 PR 09-APR-1999; 99US-00289198.
 PR 28-OCT-1999; 99US-00429755.
 PR 23-MAR-2000; 2000US-00534825.
 PR 24-MAY-2000; 2000US-00577505.
 PR 08-JUN-2000; 2000US-00590583.
 PR 26-OCT-2000; 2000US-00599295.
 PR 16-MAR-2001; 2001US-00810936.
 XX (FRUD//) FRUDAKIS T N.
 PA (REED//) REED S G.
 PA (SMITH//) SMITH J M.
 PA (MISH//) MISHNER L E.
 PA (DILL//) DILLON D C.
 PA (RETT//) RETTER M W.
 PA (WANG//) WANG A.
 PA (SKEI//) SKEIKY Y A W.
 PA (HARL//) HARLOCKER S L.
 PA (DAYC//) DAY C H.
 PA (LISX//) LI S X.
 PA (DENG//) DENG T.
 XX Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
 PI Wang A, Skeiky YAW, Harlocker SL, Day CH, Li SX, Deng T;
 XX WPI: 2003-247262/24.
 XX P-PSDB; ADA11394.

XX New breast tumor proteins nucleic acids encoding such proteins, useful in
 PT diagnosing, preventing and/or treating diseases such as cancer,
 PT particularly breast cancer, and as markers for detecting the presence of
 PT a cancer.

XX Claim 1; Page 149; 190pp; English.

XX The invention relates to a breast tumour polynucleotide selected from one
 CC of the 275 fully defined nucleotide sequences (a) given in the
 CC specification, including their complements, sequences consisting of at
 CC least 20 contiguous residues of a sequence in (a), sequences that
 CC hybridise to a sequence in (a) under moderately stringent conditions,
 CC sequences having at least 75% or 90% identity to a sequence in (a), or
 CC degenerate variants of a sequence in (a). Also included are an isolated
 CC polypeptide (ii) comprising an amino acid sequence selected from
 CC sequences encoded by (a), sequences having at least 70% or 90% identity
 CC to a sequence encoded by (a), sequences of 30 fully defined amino acid
 CC sequences (c), and sequences having at least 70% or 90% identity to a
 CC sequence in (c), expression vectors comprising (a), a host cell
 CC transformed or transfected with the expression vector, an isolated
 CC antibody or its antigen-binding fragment that specifically binds to (ii),
 CC a method for detecting the presence of a cancer in a patient, a fusion
 CC protein comprising at least one polypeptide (ii), an oligonucleotide that
 CC hybridises to (a), under moderately stringent conditions, a method for
 CC stimulating and/or expanding T cells specific for a tumour protein (by

CC contacting T cells with at least one component selected from (a), (ii)
CC and antigen-presenting cells that express (ii)), an isolated T cell
CC population comprising T cells prepared from as detailed above, a method
CC for stimulating an immune response or treating cancer in a patient by
CC administering a composition comprising (a), (ii), the vector, cells or
CC the antibodies, and a method for inhibiting the development of a cancer
CC in a patient. The polynucleotides may be used in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in tumour cells. The breast tumour proteins are
CC useful as markers to indicate the presence or absence of a cancer, such
CC as breast cancer, and in the detection of other cancers. Compositions
CC comprising the breast tumour proteins are useful in diagnosing,
CC preventing and/or treating diseases such as cancer, particularly breast
CC cancer. The present sequence is a breast cancer specific cDNA of the
CC invention.

XX Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;

Query Match 89.2%; Score 831.8; DB 7; Length 879;
Best Local Similarity 99.8%; Pred. No. 1.4e-238;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGCAAGAGCAAGCTGGGCACTTCTGGAGACCACCAAGCACTCTCTGTGAA 158
DB 42 CAGGGGAGCGGCAAGAGCAAGCTGGGCACTTCTGGAGACCACCAAGCACTCTCTGTGAA 101
QY 159 GAGCCTTTGGAGCAAGAGGTGCAAGTGGTCTGCCACTGCTTCCCTGTGAGGGGGAG 218
DB 102 GAGCCTTTGGAGCAAGAGGTGCAAGTGGTCTGCCACTGCTTCCCTGTGAGGGGGAG 161
QY 219 CGGCAAGAGCAAGCTGGGCGCTGGGGAGACTAGATGACAGCGCTTCATGATCCCAAG 278
DB 162 CGGCAAGAGCAAGCTGGGCGCTGGGGAGACTAGATGACAGCGCTTCATGATCCCAAG 221
QY 279 GTACCAAGCTCCATGGAGAGATCTGGCAAGCTCCACAGAGCTGCTGTGGGTAAAGT 338
DB 222 GTACCAAGCTCCATGGAGAGATCTGGCAAGCTCCACAGAGCTGCTGTGGGTAAAGT 281
QY 339 CCCGAGAAAGATCTATCTCATCTGCTCAGGACACTGATGTAACAAGAGGACAGCA 398
DB 282 CCCGAGAAAGATCTATCTCATCTGCTCAGGACACTGATGTAACAAGAGGACAGCA 341
QY 399 AAGAGAGCTGCTTACATCTGGCCTCTGCAATGGGAATTCAGAACTAGTAAATCTGT 458
DB 342 AAGAGAGCTGCTTACATCTGGCCTCTGCAATGGGAATTCAGAACTAGTAAATCTGT 401
QY 459 GCTGGACAGACGATGTCAACTTAATGTCTTGACCAACAAAGAGACAGCTCTGCACAA 518
DB 402 GCTGGACAGACGATGTCAACTTAATGTCTTGACCAACAAAGAGACAGCTCTGCACAA 461
QY 519 GCGGTACATGCCAGAGCAAGATGATGTGCTTAATGCTTGGACATGGCACTGATCC 578
DB 462 GCGGTACATGCCAGAGCAAGATGATGTGCTTAATGCTTGGACATGGCACTGATCC 521
QY 579 AAATATTCCAGATGATGGAATATCCATCTACACTATGCTGTCTACAAATGAATAA 638
DB 522 AAATATTCCAGATGATGGAATATCCATCTACACTATGCTGTCTACAAATGAATAA 581
QY 639 ATTAATGCCAAGACATGCTTATACGCTGCTGATATCGATCAAAACAGCATGG 698
DB 582 ATTAATGCCAAGACATGCTTATACGCTGCTGATATCGATCAAAACAGCATGG 641
QY 699 CCTCACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTAAAT 758
DB 642 CCTCACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTAAAT 701
QY 759 CAAGAAAAAGCGAATTTAAATGGCGCTGGATAGATAGGAAGAACTGCTCTCATCTTC 818
DB 702 CAAGAAAAAGCGAATTTAAATGGCGCTGGATAGATAGGAAGAACTGCTCTCATCTTC 761
QY 819 TGTATGTTGGATCAGCAAGTATAGTCAGCGCTCTACTTGAGCAAAATGTTGATGATC 878
DB 762 TGTATGTTGGATCAGCAAGTATAGTCAGCGCTCTACTTGAGCAAAATGTTGATGATC 821

QY 879 TTCTCAAGATCTGGAAGACGCGCAGAGAGTATGCTGTTTCTAGTCATCATG 933
DB 822 TTCTCAAGATCTGGAAGACGCGCAGAGAGTATGCTGTTTCTAGTCATCATG 876

RESULT 15
ADC15366

ID ADC15366 standard; DNA; 879 BP.

XX AC ADC15366;

XX DT 18-DEC-2003 (first entry)

XX DE Human breast tumour protein DNA, SEQ ID 314.

XX KW Cytostatic; Gene therapy; breast cancer; breast tumour protein; human; ds.

XX OS Homo sapiens.

XX PN WO2003013431-A2.

XX PD 20-FEB-2003.

XX PF 05-AUG-2002; 2002WO-US024917.

XX PR 07-AUG-2001; 2001US-00924400.

XX PR 20-FEB-2002; 2002US-00079137.

XX PR 02-AUG-2002; 2002US-00212679.

XX PA (CORI-) CORIXA CORP.

XX PI Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH; Kalos MD;

XX DR WPI; 2003-342398/32.

XX PT New polynucleotide, useful for preparing a composition for diagnosing, treating or preventing cancer.

XX PS Example 1; SEQ ID NO 314; 308pp; English.

XX The present invention relates to compositions and methods for the therapy and diagnosis of cancer, particularly breast cancer. The method for detecting the presence of a cancer in a patient comprises: obtaining a biological sample from the patient; contacting the biological sample with a binding agent that binds to the polypeptide; detecting in the sample an amount of the polypeptide that binds to the binding agent; and comparing the amount of the polypeptide to a predetermined cut-off value. Treating breast cancer comprises administering a composition comprising breast tumour proteins and nucleic acids, which stimulates and/or expands T cells specific for the tumour protein. The present sequence was used to illustrate the invention.

XX SQ Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;

Query Match 89.2%; Score 831.8; DB 9; Length 879;

Best Local Similarity 99.8%; Pred. No. 1.4e-238;

Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGCAAGAGCAAGCTGGGCACTTCTGGAGACCACCAAGCACTCTCTGTGAA 158
DB 42 CAGGGGAGCGGCAAGAGCAAGCTGGGCACTTCTGGAGACCACCAAGCACTCTCTGTGAA 101
QY 159 GACGCTTGGAGCAAGAGGTGCAAGTGGTGTGCTTCCCTGCTGAGGGGGAG 218
DB 102 GACGCTTGGAGCAAGAGGTGCAAGTGGTGTGCTTCCCTGCTGAGGGGGAG 161
QY 219 CGGCAAGAGCAAGCTGGGCGCTGGGGAGACTAGATGACAGCGCTTCATGATCCCAAG 278
DB 162 CGGCAAGAGCAAGCTGGGCGCTGGGGAGACTAGATGACAGCGCTTCATGATCCCAAG 221

[illegible]

Search completed: April 30, 2004, 11:22:37
Job time : 430 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 11:07:17 ; Search time 2524 Seconds
(without alignments)
11038.595 Million cell updates/sec

Title: US-10-079-137b-343

Perfect score: 933

Sequence: 1 atggtgttgagggttgattc.....tggttttagtcatcatg 933

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmus:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_nam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	541	58.0	621	12	BM763942 K-EST0045
2	540	57.9	633	12	BM763453 K-EST0044
3	395.6	42.4	729	13	BU930826 AGENCOURT
4	390.8	41.9	865	10	BF676987 602084215

5	376.4	40.3	505	13	EX492731
6	349.2	37.4	992	13	EX437445
7	342.4	36.7	843	9	AU120666
8	331.2	35.5	544	9	AL703938
9	315.2	33.8	1020	12	BM469654
10	274	29.4	2285	11	BC038951
11	264	28.3	539	9	AA910780
12	260.8	28.0	3443	11	BC028407
13	259.2	27.8	1079	12	BM548157
14	256.8	27.5	760	13	BU568215
15	253.6	27.2	754	12	BI871077
16	249.6	26.8	1961	11	AK087771
17	249.2	26.7	537	12	BM511319
18	248	26.6	1347	11	AK084890
19	248	26.6	1758	11	AK017783
20	227.6	24.4	380	10	BF32652
21	219.2	23.5	956	13	BY171578
22	217.6	23.3	802	13	BQ432733
23	214	22.9	958	12	BI828139
24	214	22.9	1025	12	BM554194
25	213	22.8	747	12	BG717440
26	211	22.6	748	12	BI831866
27	210.2	22.5	810	12	BG703856
28	208.4	22.3	802	13	BU853535
29	208.4	22.3	856	12	BI830348
30	208	22.3	907	12	BG721483
31	207.6	22.3	743	12	BI826430
32	206.8	22.2	828	12	BI827177
33	206.8	22.2	1558	12	BM555510
34	206.4	22.1	781	12	BI560539
35	206.2	22.1	808	12	BI549417
36	206	22.1	864	12	BI831391
37	204.6	21.9	916	12	BG716974
38	203.2	21.8	830	12	BI520473
39	202.4	21.7	899	12	BI546858
40	202.2	21.7	1554	11	AK015948
41	200.8	21.5	755	13	BU852157
42	200.8	21.5	845	13	BU569542
43	199.2	21.4	694	12	BG720647
44	199.2	21.4	872	12	BI831462
45	197.4	21.2	791	12	BG719053

ALIGNMENTS

RESULT 1
BM763942
LOCUS K-EST0045367 S13KMS5 Homo sapiens cDNA clone S13KMS5-25-A11 5',
DEFINITION mRNA sequence.
ACCESSION BM763942
VERSION BM763942.1 GI:19093557
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 621)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsungemail.kribb.re.kr
Plate: 25 row: A column: 11
High quality sequence stop: 621.

621 bp mRNA linear EST 04-MAR-2002

FEATURES

Location/Qualifiers
1. 621
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS5-25-All"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10F"
/clone_lib="S13KMS5"
/note="vector: PCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 58.0%; Score 541; DB 12; Length 621;
Best Local Similarity 100.0%; Pred. No. 1.6e-125; Indels 0; Gaps 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 393 CAAGCAAAAGAGGACTGCTTACATCTGGCTCTGCCAATGGGAATTCAGAACTAGTAAA 452
DB 1 CAAGCAAAAGAGGACTGCTTACATCTGGCTCTGCCAATGGGAATTCAGAACTAGTAAA 60
QY 453 ACTGCTGTCGACAGAGATGTCACCTTAATGTCCTTGACCAACAAAGAGGACGCTCT 512
DB 61 ACTGCTGTCGACAGAGATGTCACCTTAATGTCCTTGACCAACAAAGAGGACGCTCT 120
QY 513 GACAAAGCCGTCACATGCCAGGAAGATGAATGTGCGTTAATGTGTCGAAACATGGCAC 572
DB 121 GACAAAGCCGTCACATGCCAGGAAGATGAATGTGCGTTAATGTGTCGAAACATGGCAC 180
QY 573 TGATCCAAATATTCAGATGATGGAATGGAATACCACTTACATGCTGCTTACAAATGA 632
DB 181 TGATCCAAATATTCAGATGATGGAATGGAATACCACTTACATGCTGCTTACAAATGA 240
QY 633 AGATAAATTAATGCCAAAGCACTGCTTATACGGTGGCTGATCGAATCAAAACAA 692
DB 241 AGATAAATTAATGCCAAAGCACTGCTTATACGGTGGCTGATCGAATCAAAACAA 300
QY 693 GCATGGCTCACACCACTGCTTATGATATACATGACCAAAACAGCAAGTGTGAAT 752
DB 301 GCATGGCTCACACCACTGCTTATGATATACATGACCAAAACAGCAAGTGTGAAT 360
QY 753 TTTAATCAAGAAAAGCGAATTTAATGCGCTGGATAGATGGAAGAACTGCTTCAT 812
DB 361 TTTAATCAAGAAAAGCGAATTTAATGCGCTGGATAGATGGAAGAACTGCTTCAT 420
QY 813 ACTTGCTGTATGTTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGA 872
DB 421 ACTTGCTGTATGTTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGA 480
QY 873 TGTATCTTCTCAAGATCTGGAAGACCGCAGAGATGCTGTTTCTAGTCATCATCAT 932
DB 481 TGTATCTTCTCAAGATCTGGAAGACCGCAGAGATGCTGTTTCTAGTCATCATCAT 540
QY 933 G 933
DB 541 G 541

RESULT 2

BM763453
LOCUS
DEFINITION
X-EST0044791 S13KMS5 Homo sapiens cDNA clone S13KMS5-16-All 5', linear mRNA 633 bp EST 04-MAR-2002
BM763453
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 633)
AUTHORS
Oh,K.N., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Kim,Y.S., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001
UNPUBLISHED (2002)
CONTACT: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 16 row: A column: 11
High quality sequence stop: 633.
Location/Qualifiers
1. 633
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS5-16-All"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10F"
/clone_lib="S13KMS5"
/note="vector: PCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

FEATURES

Source
1. 633
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS5-16-All"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10F"
/clone_lib="S13KMS5"
/note="vector: PCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 57.9%; Score 540; DB 12; Length 633;
Best Local Similarity 99.8%; Pred. No. 2.8e-125;
Matches 540; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 393 CAAGCAAAAGAGGACTGCTTACATCTGGCTCTGCCAATGGGAATTCAGAACTAGTAAA 452
DB 1 CAAGCAAAAGAGGACTGCTTACATCTGGCTCTGCCAATGGGAATTCAGAACTAGTAAA 60
QY 453 ACTCGTGTGGACAGACGATGTCACCTTAATGTCCTTGACCAACAAAGAGGACAGCTCT 512
DB 61 ACTCGTGTGGACAGACGATGTCACCTTAATGTCCTTGACCAACAAAGAGGACAGCTCT 120
QY 513 GACAAAGCCGTCACATGCCAGGAAGATGAATGCGTTAATGTGCTGGAACATGGCAC 572
DB 121 GACAAAGCCGTCACATGCCAGGAAGATGAATGCGTTAATGTGCTGGAACATGGCAC 180
QY 573 TGATCCAAATATTCAGATGATGGAATGGAATACCACTTACATGCTGCTTACAAATGA 632

```
Db 181 TGATCCAAATATCCAGATGAGTGAATGAAATACCACTCTACACTATGCTGTCTACAATGA 240
Qy 633 AGATAAATTATGCGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAA 692
Db 241 AGATAAATTATGCGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAA 300
Qy 693 GCATGGCTCACACACTGCTTACTTGTGTATACATGAGCAAAAAACAGCAAGTGTGAATT 752
Db 301 GCATGGCTCACACACTGCTTACTTGTGTATACATGAGCAAAAAACAGCAAGTGTGAATT 360
Qy 753 TTTAATCAAGAAAAAGCGAATTTAAATGCGCTGGATAGATAGAAAGAACTGCTTCAT 812
Db 361 TTTAATCAAGAAAAAGCGAATTTAAATGCGCTGGATAGATAGAAAGAACTGCTTCAT 420
Qy 813 ACTTGCTGTATGTTGGATCAGCAAGATATAGTCAGCCCTCTACTTGCAGCAAAATGTTGA 872
Db 421 ACTTGCTGTATGTTGGATCAGCAAGATATAGTCAGCCCTCTACTTGCAGCAAAATGTTGA 480
Qy 873 TGTATCTTCTCAAGATCTGGAAGACGCCAGAGAGATGCTGTTCTAGTCATCATCAT 932
Db 481 TGTATCTTCTCAAGATCTGGAAGACGCCAGAGAGATGCTGTTCTAGTCATCATCAT 540
Qy 933 G 933
Db 541 G 541

RESULT 3
BU930826 729 bp mRNA linear EST 18-OCT-2002
LOCUS AGENCOURT_10425351 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:6668956
DEFINITION 5', mRNA sequence.
ACCESSION BU930826
VERSION BU930826.1 GI:24119645
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 729)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiCM2943 row: 0 column: 04
High quality sequence stop: 555.
Location/Qualifiers
1..729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6668956"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_83"
/note="Organ: prostate; Vector: pDNR-LTB (Clontech);
Site1: SfII (ggcgctcgccg); Site2: SfiI
(ggcatatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CAGGCCATATGACC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGGCGGCATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."
```

ORIGIN

```
Query Match 42.4%; Score 395.6; DB 13; Length 729;
Best Local Similarity 90.5%; Pred. No. 8.9e-89;
Matches 458; Conservative 0; Mismatches 14; Indels 34; Gaps 2;
Qy 462 GGACAGAGCATCTCAACTTAATGCTCTTACAAACAAAGAGGACAGCTCTCTGACAA--- 517
Db 3 GGACAGAGCATCTCAACTTAATGCTCTTACAAACAAAGAGGACAGCTCTCTGATAAGGT 62
Qy 518 -----AGCCCGTACAATGCCAGGAAGATGAATGCGGTT 551
Db 63 ATGCAGTACCCAACTATATCAGCATGAGCGCGTACAATGCCAGGAAGATGAATGCGGTT 122
Qy 552 AATGTTGCTGGAAACATGGCACTGATCCAAATATTCAGATGATGATGGAATACCACTCT 611
Db 123 AATGTTGCTGGAAACATGGCACTGATCCAAATATTCAGATGATGATGGAATACCACTCT 182
Qy 612 ACACATATGCTGTCTCAATGAAGATAAAATTAATGCCAAAGCACTGCTCTTATACGGTGC 671
Db 183 GCACATAGCTATCTATATGAAGATAAAATTAATGCCAAAGCACTGCTCTTATACGGTGC 242
Qy 672 TGATATCGAATCAAAAAACAGCATGGGCTCACACACTGCTTACTTGGTATACATGAGCA 731
Db 243 TGATATCGAATCAAAAAACAGCATGGGCTCACACACTGCTTACTTGGTATACATGAGCA 302
Qy 732 AAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCGCTGGATAG 791
Db 303 AAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCGCTGGATAG 362
Qy 792 ATATGGAAGAACTGCTCTCATACTTGTGTATGTTGTGGATCAGCAAGATATAGTCAGCCC 851
Db 363 ATATGGAAGAACTGCTCTCATACTTGTGTATGTTGTGGATCAGCAAGATATAGTCAGCCC 422
Qy 852 TCTACTTGGAGCAAAATGTTGATGATCTCTCAAG---ATCTGGAAGACGCGCCAGAGA 907
Db 423 TCTACTTGGAGCAAAATGTTGATGATCTCTCAAGATCTCTTCAAGATCTCTGACAGACGCGCCAGAGA 482
Qy 908 GTATGCTGTTTCTAGTCATCATCATG 933
Db 483 GTATGCTGTTTCTAGTCATCATCATG 508
```

RESULT 4

```
BF676987 865 bp mRNA linear EST 21-DEC-2000
LOCUS 602084215F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248746 5',
DEFINITION mRNA sequence.
ACCESSION BF676987
VERSION BF676987.1 GI:11950882
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 865)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiCM1067 row: m column: 03
High quality sequence stop: 642.
Location/Qualifiers
1..865
/organism="Homo sapiens"
```


JOURNAL
COMMENT

Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5500.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0CAP006DF02P1&cluster=5500.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0CAP006DF02P1.

FEATURES
source

Location/Qualifiers
1..992
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP006Y104"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/notes="Vector: pCMVSPORT 6, 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Query Match 37.4%; Score 349.2; DB 13; Length 992;
Best Local Similarity 68.9%; Pred. No. 5.5e-77;
Matches 496; Conservative 1; Mismatches 214; Indels 9; Gaps 1;

QY 106 AGCGGCAAGAGCAAGCTGGGCACTCTGGAGACCACAAAGCTCTCTGTGAAGAGCTT 165
DB 182 AGAGCCGAGAGACATAGAGTGTCTGAAGCCGGTGCCTGGGCCATGAAGAGATT 241
QY 166 GGAGCAAGAGTGCAGTGGTGTCTCCCACTGCTTCCCTGTGCGAGGGAGCGCAAG 225
DB 242 TTTAGTAAGAAAGCGAGTGGCCCTTGGCTCTCTTCG-----GGCGCGGGAGG 292
QY 226 AGCAAGCTGGCGCTTGGGAGACTAGATGACAGCGCTTCTATGATCCAGGTACCAC 285
DB 293 AGCAGCGCGGAGCGCGGGGCGAGCGGGGAGGGCGCTATCGCAGCGCGGTACCAC 352
QY 286 GTCCATGAGAGAGATCGGACAGCTCCACAGAGCTGCTGTGGGTAAAGTCCGCCAGA 345
DB 353 GTCCGAGCCGAGATCTCGCAAGATCCACAAAGTCCAGCGCGGTAAATGTGGCGAA 412
QY 346 AAGGATCTATGCTATGCTCAGGACACTGATGTGAACAAGAGGACAAAGAGG 405
DB 413 GTGCAGCAGATCTTTTGTCTAGGAAGATGGCTTGAACGATAGAGCAAGATGAACAG 472
QY 406 ACTGCTCTACATCTGCGCTCTGCAATGGGAATTCAGAAAGTAGTAAACTGCTGCTGGAC 465
DB 473 ACGGCTCTACATTTGGCTGTGCCATGTCTATCAGAAAGTAGTAACTCTCTGCTGGAC 532
QY 466 AGACGATGCTCAATTAATGTCTTGAACAACAAAGAGAGGACAGCTTGAACAAGCCGTA 525
DB 533 AGAAATGCGCAGTCAATGCTGTGACAAACGAAACAGGACAGCTCTGATGAAGCTGTA 592
QY 526 CAATGCCAGAGATGAATGCGTTAATGTGTGGACATGGCACTGATCCCAATATT 585
DB 593 CAATGCCAGAGAGAAATGTGCAACTATCTGTGTAAGACATGGTGTGATCCAAATCTT 652
QY 586 CCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTAACAATGAAGATAAATTAATG 645
DB 653 GCGGATGTCATGGCAACACTGCTCTTCACTATGCTGTCTAATAATGAGACATATCAGTA 712
QY 646 GCCAAGACATGCTCTTATACGGTGTGATATGCAATCAAAAAACAGCATGGCTCACA 705
DB 713 GCAACAAGACTGCTTTTGTATGATGCAATATTTGAAGCAAAAAACAGGATGACCTACA 772
QY 706 CCAGTCTACTTGGTATATAGCAAGAAAAACAGCAAGTGGTGAATTTTAAATCAAGAA 765

Db

773 CCACCTTTTACTTGCAGTAAGTGAARAGCAGCAATGGTGAATTTTAAATAAGAAA 832
QY 766 AAAGCGAATTTAAATGCGCTGATAGATATGGAAGACTGCTCTCATACTTGTGTATGT 825
DB 833 AAAGCAATGTAATGCAAGTGTGAAGTGGAAAGCAGTCCACCAACTAATTTTCAAGATAT 892

RESULT 7

AUI20666

LOCUS AUI20666 HEMBB1 Homo sapiens cDNA clone HEMBB1001175 5', mRNA
DEFINITION sequence.
ACCESSION AUI20666
VERSION AUI20666.1 GI:10935901
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS

Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

TITLE

JOURNAL

COMMENT

FEATURES
source

Location/Qualifiers
1..843
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEMBB1001175"
/tissue_type="whole embryo, mainly body"
/dev_stage="embryo, 10 weeks"
/clone_lib="HEMBB1"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 36.7%; Score 342.4; DB 9; Length 843;
Best Local Similarity 68.6%; Pred. No. 2.6e-75;
Matches 488; Conservative 0; Mismatches 214; Indels 9; Gaps 1;
QY 106 AGCGGCAAGAGCAAGCTGGGCACTCTGGAGACCACAAAGCTCTCTGTGAAGAGCTT 165
DB 119 AGAGCCGAGAGACATAGAGTGTCTCTGAAGCCGGTGCCTGGGCCATGAAGAGATT 178
QY 166 GGGAGCAAGAGTGTGCAAGTGTGCTGCCACTGCTTCCCTGTGTCAGGGGGAGCGCAAG 225
DB 179 TTTAGTAAGAAAGCGAGTGGCCCTTGGGCTCTTCG-----GGCGCGGGAGG 229
QY 226 AGCAAGCTGGCGCTTGGGAGACTTCAATGACAGCGCTTCAATGATCCAGGTACCAC 285
DB 230 AGCAGCGCGGAGCGCGGGGCGAGCGGGGAGGGCGCTTACTCGCAGCGCGGTACCAC 289
QY 286 GTCCATGAGAGATCTGGAACAAGCTCCACAGAGCTGCTTGGTGGGTAAAGTCCCCAGA 345
DB 290 GTCCGAGCCGAGATCTCGCAAGATCCACAAAGTCCAGCGCGGTAAATGTGGCGAAA 349
QY 346 AAGGATCTCATGCTCATGCTCAGGACACTGATGTGAACAAGAGGGGACAAAGCAAGAGG 405
DB 350 GTGCAGCAGATCTCTTTTGTCTCAGGAAGATGGCTTGAACCGATAGACAAAGATGAACAGG 409

QY 406 ACTGCTTACATCTGCGCTTCCGATGGGAATTCAGAGTAGTAATAACTCGTGTGGAC 465
DB 410 ACGGCTTCTACATTTGGCCCTGTCGCAATGGTCAATCAGAGTAGTAATCTCTCTGTGGAC 469
QY 466 AGACGATGTCAACTTAATCTCTTGTGACACAAAGAGGACAGCTCTCTGACAAAGCCGTA 525
DB 470 AGAAATGCGCAGCTCAATCTCTGTGACACAAAGAGGACAGCTCTCTGATGAAGCTGTA 529
QY 526 CAATGCCAGGAGAGTAATGCTGCTTAATGCTGCTGGAACATGCGACATGATCCCAATATT 585
DB 530 CAATGCCAGGAGAGTAATGCTGCTTAATGCTGCTGGAACATGCGACATGATCCCAATATT 589
QY 586 CCAGATGATGGAATACCACTCTACACTATGCTGCTCAATCAAGATAAATAATG 645
DB 590 GCGATGTCATGCGCAACTGCTCTTCACTATGCTGCTCAATCAAGATAAATAATG 649
QY 646 GCCAAGCACTGCTTATACGGTGTGATGATGCAATCAAAAGAGGACAGCTCTGAC 705
DB 650 GCAACAAAGCTGCTTATGATGCAATATGAAAGCAAAAGAGGACAGCTCTGAC 709
QY 706 CCACTCTACTTGGTATATACATGAGCAAAAGAGGACAGCTCTGCAATCAAGATAAATAATG 765
DB 710 CCATTTTACTTGCAAGTAGTGGAAAGAGGACAGCTCTGCAATCAAGATAAATAATG 769
QY 766 AAGCGAATTTAAATGCGGTGATGATGATGCAATCAAAAGAGGACAGCTCTGATCT 816
DB 770 AAGCAAAATGTAATGCCNTANATAAGTTGGAAGAGGACAGCTCAACCAATTT 820

RESULT 8
AL703938 544 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp686E1728_r1 686 (synonym: hlc3) Homo sapiens cDNA clone
DEFINITION DKFZp686E1728 5', mRNA sequence.
ACCESSION AL703938
VERSION AL703938.1 GI:19687293
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 544)
AUTHORS Ottenwaelder, B., Obermaier, B., Mewes, H.W., Mewes, H.W., Weil, B. and
Wiemann, S.
TITLE EST (Ottenwaelder, B., Obermaier, B., Mewes, H.W., Weil, B. and
Wiemann, S.)
JOURNAL Unpublished (2001)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No sl sequence
available.
This clone (DKFZp686E1728) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source
1..544
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686E1728"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pTriplEx2; Site_1: sfIIA; Site_2: SfiIB;
cDNA-collection"

Query Match 35.5%; Score 331.2; DB 9; Length 544;

Best Local Similarity 91.9%; Pred. No. 1.4e-72;
Matches 373; Conservative 0; Mismatches 28; Indels 5; Gaps 2;
QY 532 CAGGAAGATGAATGTCGTTAAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGAT 591
DB 1 CAGGAAGATGAATGTCGTTAAATGTTGCTGGAACATGGCCGATGGAATATTCAGAT 60
QY 592 GAGTATGGAATACCACTCTACACTATGCTCTACAAATGAAGATAAATTAATGGCCAAA 651
DB 61 GAGTATGGAATACCACTCTACACTAT-CTATCTCAATGAAGATAAATTAATGGCCAAA 119
QY 652 GCACCTGCTCTTATACGCTGCTGATATCGAATCAAAAAACAAGCATGGCCCTCACACCACTG 711
DB 120 GCACCTGCTCTTATGCTGCTGATATGAATCAAAAAACAAGCTGGCCCTCACACCACTT 179
QY 712 CTACTTGGTATACATGAGCAAAACAGCAAGTGGTGAATTTTAATCAAGAAAAAAGCG 771
DB 180 TTGCTGGCGTGCATGAACAAAAACAGGAAGTGGTGAATTTTAATCAAGAAAAAAGCT 239
QY 772 AATTAAATCGCTGGATAGATATGAAGAACTGCTCTCATCTGCTGATCTGTTGTTGGA 831
DB 240 AATTAAATCGCTGGATAGATATGAAGAACTGCTCTCATCTGCTGATCTGTTGTTGGA 299
QY 832 TCAGCAAGTATAGTACGCCCTCTACTTGAGCAAAATGTTGATGATATCTTCTCAAG---A 887
DB 300 TCAGCAAGTATAGTCAATCTTCTACTTGAGCAAAATGTTGATGATATCTTCTCAAGATCTA 359
QY 888 TCTGGAAAGACGCCGACAGAGATGCTGTTCTTAGTCATCATCATG 933
DB 360 TCTGGACAGAGCCGACAGAGATGCTGTTCTTAGTCATCATCATG 405

RESULT 9
BM469654 1020 bp mRNA linear EST 05-FEB-2002
LOCUS AGENCOURT 644673 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5585453
DEFINITION 5', mRNA sequence.
ACCESSION BM469654
VERSION BM469654.1 GI:18518696
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1020)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ARCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12351 row: m column: Q6
High quality sequence stop: 680.
Location/Qualifiers
1..1020
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5585453"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dr primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

FEATURES
source
1..1020
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5585453"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dr primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 33.8%; Score 315.2; DB 12; Length 1020;
 Best Local Similarity 73.7%; Pred. No. 2.4e-66;
 Matches 401; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

Qy 282 CCAGTCCATGGAGAGATCTGGACAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCC 341
 Db 1 CCAGTCCGAGACGAGATCTGGCAAGATCCCAAGCTGCCAGCGCGGTAAATGTGGC 60

Qy 342 CAGAAAGATCTCATCTCATCTCAGGACATGATGTGAACAAGGAGGACAGCAAA 401
 Db 61 GAAAGTCCAGCAGATCTTTTGTCCAGAAAGATGGCTTGAACGATAGACAGATGAA 120

Qy 402 GAGGACTGCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 461
 Db 121 CAGACGGCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180

Qy 462 GGACAGAGATGTCAACTTAATGTCCTTGACACAAAGAGAGACAGCTCTGCAAGGC 521
 Db 181 GGACAGAAATGCCAGCTCAATGTCTGTGACACGAAACAGGACAGCTCTGATGAAGC 240

Qy 522 CGTCAATGCCAGAGATGAATGTGCTTAATGTTCTGCAATGGCACTGATCCAAA 581
 Db 241 TGTCAATGCCAGAGAGAAATGTCAATTTCTCTAGAACATGCTGCTGCTGCTGCT 300

Qy 582 TATTCAGATGATGGAATATCACTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 641
 Db 301 TCTTGGGATGCTCCATGCAACACTGCTCTTCACTATGCTGCTGCTGCTGCTGCTGCT 360

Qy 642 AATGCCAAAGCATGCTCTTATAGCTGCTGATATGATATGATATGATATGATATGAT 701
 Db 361 AGTAGCAACAAAGCTGCTTTTGTATGATGCAATATTGTAAGCAAAACAGGATGACCT 420

Qy 702 CACACCACTGCTACTTGTGTATACATGACGCAAAACAGCAAGTGGTGAATTTTATCAA 761
 Db 421 CACACCACTTTTCTGAGTGAAGAAAGAGCAAGTGGTGAATTTTATCAA 480

Qy 762 GAAAGAGCAATTAATGCTGCTGATATGATATGATATGATATGATATGATATGAT 821
 Db 481 GAAAGAGCAATTAATGCTGATATGATATGATATGATATGATATGATATGATATGAT 540

Qy 822 ATGT 825
 Db 541 ATAT 544

RESULT 10
 BC038951
 LOCUS
 DEFINITION Homo sapiens ankyrin repeat domain 19, mRNA (CDNA clone IMAGE:5733799), with apparent retained intron.
 ACCESSION BC038951
 VERSION BC038951.1 GI:25058320
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (Bases 1 to 2285)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, J., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Narusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Tishiyuki, S., Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Wyers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smillie, D.E., Schnerf, A., Schein, J.E., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 2285)
 Strausberg, R.
 Direct Submission
 Submitted (01-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Invitrogen
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@hgri.nih.gov
 Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripo, S., Thomas, P.J., Touchman, J.W., Tsourgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 82 Row: i Column: 11
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Genomescan gene prediction
 This clone has the following problem: retained intron.

FEATURES
 Location/Qualifiers
 1..2285
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5733799"
 /tissue_type="Brain, hippocampus"
 /clone_lib="NIH MGC_124"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 29.4%; Score 274; DB 11; Length 2285;
 Best Local Similarity 63.6%; Pred. No. 8.2e-58;
 Matches 435; Conservative 0; Mismatches 245; Indels 4; Gaps 1;

Qy 247 GACTACATGACAGCGCTTCATGATCCAGTACCACCTCCATGGAGAGATCTGCATGCTC 306
 Db 103 GACTCCATGGACCAAGATGACGTGGTGGGGTACCACATCCGGGACTGGGACTGGCG 162

Qy 307 AAGCTCCACAGAGCTGCTGCTGGGTAAAGTCCCAAGAGGATCTCATGCTCATGCTC 366
 Db 163 AGATCCACAGGCTGCCATCAAGGCGCGCGGGAGTGGACACTGCCTGACGGC 222

Qy 367 AGGACACTGATGTGAACAGAGGAGCAAGCAAGAGAGACTGCTCTACATCTGCCTCT 426
 Db 223 AGGTTCCGGGACTTCGACGCCCGCGACAGAAAGACAGGACTGTTCTCAATTGACCTGT 282

Qy 427 GCCAATGGGAATTCAGAAAGTAGTAAATCTCGTGTGGACAGACGATGTCAACTTAATGTC 486

Db GCCATGGCGGTGGAGTGGTCAACCTCTTCTGAGCAGAGATGCCAGATCAACATA 342
QY 487 CTTGACACAAAAGAGCAGCTCTGACAAAGCCGTACATGCCAGGAAGATGAT 546
Db 343 TATGATAGACTAAACAGGACACCTTTAATGAAGCTGTACACTGCCAGGAAGGCTTGT 402
QY 547 GCCTTAATGTTGCTGGAACATGGCACTGTATCCAAATATTCCAGATCAGTATGGAATACC 606
Db 403 GCCATTATTCTCTGGACACTGGCCCAATCCAAACATTAAGGATATCTACAGCAACT 462
QY 607 ACTCTACATATGTTCTCAATGAAGATAAATTAATGGCCAAAGCACTGCTCTTATAC 666
Db 463 GCTCTCCATTATGCTGTGTATATAAGGGGACTTCACTGCGAGAAAACCTGCTTCCAC 522
QY 667 GGTGCTGATATCAATCAAAAACACAGCATGGCTCTCACCACTGCTACTTGTGTATACAT 726
Db 523 CATGCAATATTAAGCACTTAACAGGAGGAGAAACACTCCACTTTTGTGTATTAAT 582
QY 727 GAGCAAAAACAGAGTGGTGAATTTTAAATCAAGAAAACAGGAATTAATGGCTG 786
Db 583 TCTAGGAGACAGCAAAATTTGTGAATTTCTGTTGAAGAACCCAGGCAAAATTTACATGCCAT 642
QY 787 GATGATATGGAAGACTGCTCATACTTGTGTATGTTGTGATCGACAGCACTAGTC 846
Db 643 GACAAATTCAGAGAACAGCCCTCATGCTTTCAGTACAGTAACTCATCAAGTATCGTC 702
QY 847 AGCCCTCTACTTGAGCAAAATGTTGATGATCTTCTCAAGA-----TCTGAAAAGACGGCC 902
Db 703 AGCCTCCTCTTCAACAAATATAAATATCTTTCTCAAGACCTGTTTGGCCAGACTGCC 762
QY 903 AGAGATGATGCTGTTTCTAGTCAT 926
Db 763 GAGGATTATGCTGTTTGTATAAT 786

RESULT 11
AA910780 539 bp mRNA linear EST 10-JUN-1998
LOCUS
DEFINITION O148b04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1526671 3' similar to TR:Q92527 Q92527 ANKYRIN MOTIF. 1, mRNA
sequence.
ACCESSION
VERSION AA910780
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS
TITLE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1548 Std Error: 0.00
Seq primer: -40m13 fwd. Et from Amersham
High quality sequence stop: 235.
Location/Qualifiers
1. 539
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1526671"
/lab_host="DH10B"
/clone_lib="Scarses_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and ss circles were made in

vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "

Query Match 28.3%; Score 264; DB 9; Length 539;
Best Local Similarity 72.4%; Pred. No. 1.3e-55;
Matches 356; Conservative 0; Mismatches 135; Indels 1; Gaps 1;

QY 242 GGGGAGACTACGATCAGACAGCGCCCTTCTGATCCCGATCCAGCTCCATGAGGAAGATC 301
Db 41 GGGGAGCGCGGGGAGGGCGCTTACTCGCAGCCGCGCTACCACTCCGAGCCGAGATC 100
QY 302 TGGACAAGCTCCACAGAGCTGCTGTTGGGTAAAGTCCCCAGAAAGATCTCATCTCA 361
Db 101 TCGGCAAGATCCACAAAGCTGCCAGCGGGGTAAATGTGGCGAAAGTGCAGCAGATCCTTT 160
QY 362 TGCTCAGGCACTGATGTGAACAAGAGGAGCAAGCAAGAGAGAGCTGCTTACATCTGG 421
Db 161 TGCTCAGAAAGATGGCTTGAACGATAGACACAGATGACAGGCGGCTCTCATTTGG 220
QY 422 CTTCTGCAATGGGAATTCAGAGTAGTAAACTCGTGTGGACAGAGATGTCAACTTA 481
Db 221 CTTGTG-CAATGCTCATCCAGAGTAGTAACTCTCTGTTGGACAGAAATGCGCAGTCA 279
QY 482 ATGTCCTTTGACAAACAAAAGAGGAGCAGCTCTGACAAAGGCGGTACAAATGCCAGGAAGATG 541
Db 280 ATGTCGTGACACGAAACAGGACAGCTCTGATGAGGCTGTACATGCCAGAGAGAGA 339
QY 542 AATGTCGCTTAATGTTGCTGGAACATGCACTGATCCAAATATTTCCAGATCAGATGGA 601
Db 340 AATGTGCAACTATTCTGCTAGAACATGCTGATCCAAATCTTTGCGGATCTCCATGGCA 399
QY 602 ATACCACTCTACACTATCTGCTCTACATGAAGATAAATTAATGCCAAAGCACTGCTCT 661
Db 400 ACATGCTCTTCTCATATCTGCTCTATATAGGACATATCAGTAGCAACAAGTGTCTTT 459
QY 662 TATACGCTGCTGATATCGAATCAAAAAACAGCATGGCCTCACACCACTGCTACTTGTA 721
Db 460 TGTATGATGCAAAATATTGAAGCACAAACACAGGATGACCTCACACCACTTTTACTTGCA 519
QY 722 TACATGAGCAAA 733
Db 520 TAAGTGGAAAAA 531

RESULT 12
BC028407 3443 bp mRNA linear HTC 25-NOV-2003
LOCUS
DEFINITION Homo sapiens breast cancer antigen NY-BR-1.1, mRNA (cDNA clone
IMAGE:4821910), containing frame-shift errors.
ACCESSION
VERSION BC028407
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 3443)
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.W., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carrincci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Zahedy, J., Helton, E., Ketterman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalski, U., Smal, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

REFERENCE 2 (bases 1 to 3443)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (23-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

contact: amadansystemsbio.org

Anup Madan, Jessica Fahy, Erin Helton, Mark Ketterman, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 46 Row: i Column: 20

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORP analysis

This clone has the following problem: frame shifted.

Location/Qualifiers

1. 3443

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4821910"

/tissue_type="Testis"

/clone_lib="NIH_MGC_97"

/lab_host="DH10B"

/note="Vector: pBluescript"

ORIGIN

Query Match 28.0%; Score 260.8; DB 11; Length 3443;

Best Local Similarity 65.1%; Pred. No. 2.2e-54;

Matches 401; Conservative 0; Mismatches 212; Indels 3; Gaps 1;

QY 285 CGTCCATGGAGAAGATCTGGCAAGCTCCACAGAGCTGCCTGGGGTAAAGTCCCA- 343

DB 187 CATCTACTCTGGGATCTAGGGAAGATCCATACAGCTGCCTCCGGGCCAAGTCCAGAA 246

QY 344 --GAAGAGATCTATGCTGCTCAGGGAACATGATGTGAACAAAGAGGGGCAAGCAAAA 401

DB 247 GCTGGAGAAGATGACAGTGGGGAAGACCGCTCAACCTGAACAAAAGAGATATGAAGA 306

QY 402 GAGGACTCTTACATCTGGCTCTGCCAATGGGAATTCAGAACTAGTAAACTCGTGCT 461

DB 307 GAGGACTCTTACATCTGGCTCTGCCAATGGGAATTCAGAACTAGTAAACTCGTGCT 366

QY 462 GGACAGCAGATGTCTAACTTAATGTCCTTGACACAAAAGAGGACAGCTCTGCAAAAGGC 521

DB 367 AGACAGAAAGTCCAGCTTAATGTCCTTGATGGGAGGAGGACACCTCTGATGAAGGC 426

QY 522 CGTACATGCCAGGAGATGATGTCGTTAATGTTGCTGGAACATGGCACTGATCCAAA 581

Db 427 TCTACAATGCGAGAGAGGGAGGCTTGTGCAAAATATTCTCATAGATGCTGCTGATCTAAA 486

QY 582 TATTCAGATGATGAAATACCACTTACATCTATCTCTCTACATGAAGATAAAT 641

DB 487 TTATGTAGATGATGAAACACGGCTCTCATTTATCCGTTTATAGTGAGAAATTTGT 546

QY 642 AATGCCAAAGACATCTCTTATACGGTGTGATCATCAATCAAAAACAAAGCATGGCT 701

DB 547 AATGTGGCAACACATCTCTCTATGTTGAGTCTATCGAGGTGCAAAACAGGCTAGCT 606

QY 702 CACACACTGCTACTTGTGTATACATGACAAACAGCAAGTGGTGAATTTTATCA 761

DB 607 CACACCCCTTTTACTGGCCATACAGAAAAGACGCAAACTGTGGAATTTTACTAAC 666

QY 762 GAAAAAGCAATTTAAATGCGCTGATAGATATGGAAGAACTGCTCTCATACTTGTCT 821

DB 667 AAAAAATGCAATGCAACGCATTTAATGAGTCTAATGACACAGCCCTCATGTTGCCAT 726

QY 822 ATGTTGTGATCAGCAAGTATAGTACGCTCTTACTTGGCAAAATGTTGATGATCTTC 881

DB 727 ATGTGAAGGCTCATCAGAGATAGTGGCATGCTTCTTCAGCAAAATGTTGAGCTTTC 786

QY 882 TCAAGATCTGGAAGA 897

DB 787 TGAAGACATACATGGA 802

RESULT 13

BM548157

LOCUS

DEFINITION

BM548157 1079 bp mRNA linear EST 20-FEB-2002

AGENCOURT_6571417 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5733799

5', mRNA sequence.

BM548157

VERSION

BM548157.1 GI:18782515

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1079)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Invitrogen

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Place: LLNL2738 row: b column: 08

High quality sequence stop: 632.

Location/Qualifiers

1. 1079

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5733799"

/tissue_type="hippocampus"

/lab_host="DH10B"

/clone_lib="NIH_MGC_124"

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: EcoRV (destroyed); Site 2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."

FEATURES

source

ORIGIN

```
Query Match      27.8%; Score 259.2; DB 12; Length 1079;
Best Local Similarity 63.4%; Pred. No. 3e-54;
Matches 430; Conservative 0; Mismatches 243; Indels 5; Gaps 2;

QY 247 GACTACGATCAGAGCGCTTCATGGATCCAGGTACACGCTCCATGGAGAGATCTGGAC 306
Db 114 GACTCCATGAGCAAGAGTACGCTGGTGGGGGTACACATCCGGGACTGGGAACTGGG 173
QY 307 AAGCTCCACAGAGTGCCTGGTGGGTAAAGTCCAGAAAGGATCTCATCGTCATGCTC 366
Db 174 AAGATCCACAGGCTGCCATCAAGGGGCGCGCGGAGGTGGAGCACTGCCCTGACGCG 233
QY 367 AGGACACTATGTGAACAGAGGACAGCAAAAGAGGACTCTCTAGATCTGGGCTCT 426
Db 234 AGTTCGGGACTTGGAGCGCCCGGACAGAAAGACAGGACTCTTCTAGATTGACCTGT 293
QY 427 GCCAATGGGAATTCAGAAAGTAGTAAAGTCTGCTGACAGAGAGTGTCAACTTAATGTC 486
Db 294 GCCATGCGCGTGTGGAAGTGGTCAACCTCTTCTGAGCAGAGAGTGGCCAGATCAACATA 353
QY 487 CTTCGACAAACAAAGAGGACAGCTCTGACAAAGGCGGTACAAATGCCAGGAGATGATGT 546
Db 354 TATGATAGACTAACAGGACACCTTTAATGAAGGCTGTACACTGCCAGGAGGCTTGT 413
QY 547 GCGTTAATGTTGCGAAACATGGCACTGTATCCAAATATTCAGATGAGTATGGAATACC 606
Db 414 GCCATTATCTCTGGACATGGCGCAATCCAAACATTAAGGATATCTACAGCAACT 473
QY 607 ACTCTACATATGCTGTCTCAATGAAGATAAATTAATGSCCAAGACATGCTCTTATAC 666
Db 474 GCTCTCCATATGCTGTGTATAAAGGAGCTTCACTGGCAGAAAGTCTTCTCCAC 533
QY 667 GTGCTCATATCGAATCAAAACACAGCATGGCTCACACCTGCTACTTGTGTATACAT 726
Db 534 CATGCCAATATTAAGCACTAAGAGGAGGAAACACTCCATTTTGTGTATTAAT 593
QY 727 GAGCAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAGCGAATTTAAATGCGCTG 786
Db 594 TCTAGGAGACAGCAATTTGTGAATTTCTGTGAAGAACCCAGGCAATTTACATGCCAT 653
QY 787 GATGATATGGAGAACTGCTCTCATACTGCTGTATGTTGTGATCAGCACTATAGTC 846
Db 654 GACAAATTCAGAGAAACAGCCCTCATGCTTGCAGCAGCAGCAATCACTCAAGTATGCTC 713
QY 847 AGCCCTCTACTTGAAGAAATGTTGATGTATCTTCTCAAGA---TCTGAAAGACGGCC 902
Db 714 AGCTCTCTCTTCAAC-AAATATAAATATCTTTCTCAGACCTGTTGGCCAGACTGCC 772
QY 903 AGAGATATGCTGTTTCT 920
Db 773 GAGGATTATGCTGTTTGT 790

RESULT 14
BUS68215 760 bp mRNA linear EST 16-SEP-2002
LOCUS AGENCOURT_10404547 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6615199
DEFINITION 5', mRNA sequence.
ACCESSION BUS68215
VERSION BUS68215.1 GI:22918515
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 760)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH
```

```
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2856 row: o column: 07
High quality sequence stop: 643.
Location/Qualifiers
1. 760
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6615199"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_82"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
3'f1 (ggccgctcggcc); Site_2: 5'f1 (ggccatcattgccc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATATGCGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGGCGGCGCATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

ORIGIN
Query Match      27.5%; Score 256.8; DB 13; Length 760;
Best Local Similarity 64.6%; Pred. No. 1e-53;
Matches 414; Conservative 0; Mismatches 223; Indels 4; Gaps 2;

QY 262 GCCTTATGATGCCAGGTACACGCTCCATGGAGAGATCTGGACAGCTCCACAGAGCT 321
Db 72 GCTTCGCATTTCCCATTTACTACATTAACCGTATCATCTGAAGAGGATCCACAGAGCT 131
QY 322 GCCTGGTGGGTAAAGTCCCGAGAAAGATCTCATCTCATGCTCAGGACACTGATGTG 381
Db 132 GTCTTACGTGTAACTGGAGAAACTGAA---GTACCTTCTGCTCACGTATATTAGACGCC 188
QY 382 AACAGAGGGACAAAGCAAAAGAGGACTCTCTACATCTGGCTCTGCCAATGGGAATTC 441
Db 189 ATATAGAGACAGACAGGAAGAAAGGACTGCCCTACATTTGGCTGTGCCACTGGCAACCG 248
QY 442 GAAGTAGTAAACTCGTCTGGACAGAGATGTCAACTTAATGTCTTCTTGACACAAAG 501
Db 249 GAAATGGTACATCTCTGCTGCCAGAGATGTGAGCTTAACTCTGCGACCGTGAAGAC 308
QY 502 AGGACAGCTCTGACAAAGCGCGTCAATGCCAGGAAGATGAATGCGTTAATGTTGCTG 561
Db 309 AGGACACTCTGTATCAGGCTGTACACTGAGGAGGAGGCTTGTGCACTCTTCTGCTG 368
QY 562 GAACATGCACTGATCCAAATATTCCAGATGAGTATGGAATACCACCTCTACACTATGCT 621
Db 369 CAAAATGGCGCGATCCAAATATTACGGATCTCTTTGGAAGGACTGCTCTGCACCTACGCT 428
QY 622 GTCTCAATAGAGATAAATTAATGCCAAAGCACTGCTCTTATAGCGTGTGATATCGAA 681
Db 429 GTGTATATGAAGATACATCCATGATGAGAAACTCTTCTTTCACATGGTACAAATTTGAA 488
QY 682 TCAAAAAACAAGCATGGCTCACACCTGCTACTTGTGTATATACATGAGCAAAAAACAGCAA 741
Db 489 GAATGCAGCAAGATGAATATATCAGCCACTGTACTTGTGTGAGTCGAAGAAAGTGA 548
QY 742 GTGGTGAATTTTATCAAG-AAAAAGCGAATTTAAATCGCTGGATAGATATGGAAG 800
Db 549 ATGTGGGAATTTTATTAAGAAAAAGCAATGTAATGCCATTGATTTATCTTGGCAG 608
QY 801 AACTGCTCTCATACTGCTGTGTATGTTGGATCAGCAAGTATAGTCAGCCCTCTACTTGA 860
Db 609 ATCAGCCCTCATACTGCTGTGTACTCTTTGGAGANAAGATATAGTCACTTCTTCTTCA 668
QY 861 GCAAAATGTTGATGTATCTTCTCAGATCTCGAAGACGGC 901
```

Db 669 GCACAAATATTGATGTGTTTCTCGAGATGTGTATGGAAAGC 709
|||||
BI871077 754 bp mRNA linear EST 11-Oct-2001
603394250F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5403996 5',
mRNA sequence.
BI871077
VERSION BI871077.1 GI:16044750
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 754)
NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-i@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL2030 row: d column: 13
High quality sequence stop: 729.
Location/Qualifiers
1..754
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5403996"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_90"
/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

FEATURES
source

ORIGIN

Query Match 27.2%; Score 253.6; DB 12; Length 754;
Best Local Similarity 67.2%; Pred.No. 6.6e-53;
Matches 357; Conservative 0; Mismatches 174; Indels 0; Gaps 0;
QY 356 TCGTCATGCTCAGGACACATGATGTGAACAGAGGGACAAAGAGGAGGACTGCTCTAC 415
DB 68 TCGTTCGTCTACCGCTTATGACATCAATAAGAGAGACAGAGAGGAGGACCGCCCTAC 127
QY 416 ATCTGGCCTCTGCCAATGGGAATTCAGAACTGATPAAACTCGTGTGGACAGACGATGC 475
DB 128 ATTTGGCCTGTGCGACCTGGCCACCGGAAATGGTACATCTCTGTGTCTCCAGAGATGTG 187
QY 476 AACTTAATGCTTGACAAACAAAGAGGACGCTCTGACAAAGCGCGTACATGCCAGG 535
DB 188 AGCTTAACCTCTGCGACCGGTGAACAGAGGACACCTCTGATCAAGGCTGTACAACTGAGGC 247
QY 536 AAGATGAATGTGCGTTAATGTGTGTGGAACATGGCACTGATCCAAATATTCCAGATGAGT 595
DB 248 AGGAGGCTGTGCAACTCTCTCTGTCGAAATGGCGCGATCCAAATATTACGGATGTCT 307
QY 596 ATGGAATACACATCTACACTGTCTCTACATGAAGATAAATTAATGGCCAAAGCAC 655
DB 308 TTGGAAGGACTGTCTCTGCACCTACCGCTGTGTATATGAAGATACATCCATGATAGNAAAAC 367
QY 656 TGCTCTTATACGGTGTGATATGAAATCAAAAACAAAGCATGGCCTCACACCACTGCTAC 715
|||||

Search completed: April 30, 2004, 13:07:36
Job time : 2529 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: April 30, 2004, 13:09:28 ; Search time 3747 Seconds
(without alignments)
10792.381 Million cell updates/sec
Title: US-10-079-137b-343
Perfect score: 933
Sequence: 1 atggtgttgaggttgatc.....tggttttagtcacatcatg 933
Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues
Word size : 0
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_on:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_on:*
21: em_ov:*
22: em_or:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	733	78.6	879	6	AR261059	AR261059 Sequence
2	733	78.6	879	6	AR278590	AR278590 Sequence
3	733	78.6	879	6	AR367286	AR367286 Sequence
4	733	78.6	879	6	AR400322	AR400322 Sequence
5	733	78.6	879	6	AR405589	AR405589 Sequence
6	733	78.6	879	6	AR433323	AR433323 Sequence
7	733	78.6	879	6	AR414041	AR414041 Sequence
8	733	78.6	879	6	AX200901	AX200901 Sequence
9	733	78.6	879	6	AX267557	AX267557 Sequence
10	733	78.6	879	6	AX316977	AX316977 Sequence
11	733	78.6	1852	6	AR261058	AR261058 Sequence
12	733	78.6	1852	6	AR278589	AR278589 Sequence
13	733	78.6	1852	6	AR367285	AR367285 Sequence
14	733	78.6	1852	6	AR400321	AR400321 Sequence
15	733	78.6	1852	6	AR405588	AR405588 Sequence
16	733	78.6	1852	6	AR433322	AR433322 Sequence
17	733	78.6	1852	6	AX141040	AX141040 Sequence
18	733	78.6	1852	6	AX200900	AX200900 Sequence
19	733	78.6	1852	6	AX267556	AX267556 Sequence
20	733	78.6	1852	6	AX282954	AX282954 Sequence
21	733	78.6	1852	6	AX316976	AX316976 Sequence
22	646	69.2	1851	6	AR148112	AR148112 Sequence
C 23	646	69.2	1851	6	BD424264	BD424264 Compounds
C 24	646	69.2	1851	6	AR260940	AR260940 Sequence
C 25	646	69.2	1851	6	AR278471	AR278471 Sequence
C 26	646	69.2	1851	6	AR350934	AR350934 Sequence
C 27	646	69.2	1851	6	AR350935	AR350935 Sequence
C 28	646	69.2	1851	6	AR367167	AR367167 Sequence
C 29	646	69.2	1851	6	AR371063	AR371063 Sequence
C 30	646	69.2	1851	6	AR400203	AR400203 Sequence
C 31	646	69.2	1851	6	AR405470	AR405470 Sequence
C 32	646	69.2	1851	6	AR433310	AR433310 Sequence
C 33	646	69.2	1851	6	AR433311	AR433311 Sequence
C 34	646	69.2	1851	6	AX106585	AX106585 Sequence
C 35	646	69.2	1851	6	AX140876	AX140876 Sequence
C 36	646	69.2	1851	6	AX200736	AX200736 Sequence
C 37	646	69.2	1851	6	AX267392	AX267392 Sequence
C 38	646	69.2	1851	6	AX282952	AX282952 Sequence
C 39	646	69.2	1851	6	AX316954	AX316954 Sequence
C 40	646	69.2	1851	6	AX316955	AX316955 Sequence
C 41	646	69.2	1851	6	BD084487	BD084487 Compositi
C 42	646	69.2	1851	6	BD084488	BD084488 Compositi
C 43	646	69.2	2184	6	BD242268	BD242268 Compounds
C 44	646	69.2	2184	6	AR260944	AR260944 Sequence
C 45	646	69.2	2184	6	AR278475	AR278475 Sequence

ALIGNMENTS

RESULT 1
LOCUS AR261059
DEFINITION Sequence 531 from patent US 6321716.
ACCESSION AR261059
VERSION AR261059.1 GI:28071822
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 879)
AUTHORS Mashiki, Z. and Harada, J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: US 6321716-A 531 27-NOV-2001;
FEATURES Location/Qualifiers
879 bp DNA linear PAT 29-JAN-2003

source 1..879
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 78.6%; Score 733; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGCAAGAGCAACCTGGGCACTTCTGGAGACCACACGACCTCTCTGTGAA 158
DB 42 CAGGGGAGCGGCAAGAGCAACCTGGGCACTTCTGGAGACCACACGACCTCTCTGTGAA 101

QY 159 GAGCGTTGGGAGCAAGAGGTCGAAGTGGTCTGCCACTGCTTCCCTGCTGCGAGGGGAG 218
DB 102 GAGCGTTGGGAGCAAGAGGTCGAAGTGGTCTGCCACTGCTTCCCTGCTGCGAGGGGAG 161

QY 219 CGGCAAGAGCAACCTGGGCACTTCTGGAGACCACACGACCTCTCTGTGAA 278
DB 162 CGGCAAGAGCAACCTGGGCACTTCTGGAGACCACACGACCTCTCTGTGAA 221

QY 279 GTACCAAGTCCATGGAGAGATCTGGAGAGCTCCACAGAGCTGCTGTTGGGTTAAAGT 338
DB 222 GTACCAAGTCCATGGAGAGATCTGGAGAGCTCCACAGAGCTGCTGTTGGGTTAAAGT 281

QY 339 CCCAGAGAGCAACCTGGGCACTTCTGGAGACCACACGACCTCTCTGTGAA 398
DB 282 CCCAGAGAGCAACCTGGGCACTTCTGGAGACCACACGACCTCTCTGTGAA 341

QY 399 AAGAGAGCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 458
DB 342 AAGAGAGCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 401

QY 459 GCTGGACAGAGCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 518
DB 402 GCTGGACAGAGCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 461

QY 519 AATATTTCCAGATGAGTATGGAATACCACTTACACTATGCTGTCTACAAAGAGATAA 638
DB 522 AATATTTCCAGATGAGTATGGAATACCACTTACACTATGCTGTCTACAAAGAGATAA 581

QY 639 ATTATGGCCAAAGCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 698
DB 582 ATTATGGCCAAAGCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 641

QY 699 CCTCACACCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 758
DB 642 CCTCACACCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 701

QY 759 CAAGAAAAAGCGAATTTAAATGGCTGATATGGAAGAACTGCTTCACTGCTTCACTGCTTCACTGCT 818
DB 702 CAAGAAAAAGCGAATTTAAATGGCTGATATGGAAGAACTGCTTCACTGCTTCACTGCTTCACTGCT 761

QY 819 TGTATGTTGGATCAGCAAGTATAGTACGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 878
DB 762 TGTATGTTGGATCAGCAAGTATAGTACGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 821

QY 879 TTCTCAAGATCTGGAAGAGCGGCGAGAGAGTATGCTGTTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 933
DB 822 TTCTCAAGATCTGGAAGAGCGGCGAGAGAGTATGCTGTTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 876

RESULT 2
AR278590
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

AR278590
Sequence 531 from patent US 6512094.
AR278590
AR278590.1 GI:29712836

879 bp DNA linear PAT 10-APR-2003

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 879)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6512094-A 531 28-JAN-2003;
FEATURES Location/Qualifiers
1..879
source /organism="unknown"
ORIGIN /mol_type="genomic DNA"

Query Match 78.6%; Score 733; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGCAAGAGCAACCTGGGCACTTCTGGAGACCACACGACCTCTCTGTGAA 158
DB 42 CAGGGGAGCGGCAAGAGCAACCTGGGCACTTCTGGAGACCACACGACCTCTCTGTGAA 101

QY 159 GAGCGTTGGGAGCAAGAGGTCGAAGTGGTCTGCCACTGCTTCCCTGCTGCGAGGGGAG 218
DB 102 GAGCGTTGGGAGCAAGAGGTCGAAGTGGTCTGCCACTGCTTCCCTGCTGCGAGGGGAG 161

QY 219 CGGCAAGAGCAACCTGGGCACTTCTGGAGACCACACGACCTCTCTGTGAA 278
DB 162 CGGCAAGAGCAACCTGGGCACTTCTGGAGACCACACGACCTCTCTGTGAA 221

QY 279 GTACCAAGTCCATGGAGAGATCTGGAGAGCTCCACAGAGCTGCTGTTGGGTTAAAGT 338
DB 222 GTACCAAGTCCATGGAGAGATCTGGAGAGCTCCACAGAGCTGCTGTTGGGTTAAAGT 281

QY 339 CCCAGAGAGCAACCTGGGCACTTCTGGAGACCACACGACCTCTCTGTGAA 398
DB 282 CCCAGAGAGCAACCTGGGCACTTCTGGAGACCACACGACCTCTCTGTGAA 341

QY 399 AAGAGAGCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 458
DB 342 AAGAGAGCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 401

QY 459 GCTGGACAGAGCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 518
DB 402 GCTGGACAGAGCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 461

QY 519 GGCCTCAACTGCGGCAAGATGAATGCGCTTAAATGTTGCTGGAACATGCACTGATCC 578
DB 462 GGCCTCAACTGCGGCAAGATGAATGCGCTTAAATGTTGCTGGAACATGCACTGATCC 521

QY 579 AATATTTCCAGATGAGTATGGAATACCACTTACACTATGCTGTCTACAAAGAGATAA 638
DB 522 AATATTTCCAGATGAGTATGGAATACCACTTACACTATGCTGTCTACAAAGAGATAA 581

QY 639 ATTATGGCCAAAGCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 698
DB 582 ATTATGGCCAAAGCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 641

QY 699 CCTCACACCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 758
DB 642 CCTCACACCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 701

QY 759 CAAGAAAAAGCGAATTTAAATGGCTGATATGGAAGAACTGCTTCACTGCTTCACTGCTTCACTGCT 818
DB 702 CAAGAAAAAGCGAATTTAAATGGCTGATATGGAAGAACTGCTTCACTGCTTCACTGCTTCACTGCT 761

QY 819 TGTATGTTGGATCAGCAAGTATAGTACGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 878
DB 762 TGTATGTTGGATCAGCAAGTATAGTACGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 821

QY 879 TTCTCAAGATCTGGAAGAGCGGCGAGAGAGTATGCTGTTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 933
DB 822 TTCTCAAGATCTGGAAGAGCGGCGAGAGAGTATGCTGTTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 876

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN

Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W.,
Stolk, J.A., Skeiky, Y.A., Wang, A. and Meagher, M.J.
Compositions and methods for the therapy and diagnosis of prostate
cancer
Patent: WO 0151633-A 531 19-JUL-2001;
CORIXA CORPORATION (US)
Location/Qualifiers
1. 879
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 78.6%; Score 733; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 99 CAGGGGAGCGGCAAGAGCAAGCGTGGGACATCTCGGAGACCAACGACTCTCTGTGAA 158
DB 99 |||||
QY 42 CAGGGGAGCGGCAAGAGCAAGCGTGGGACATCTCGGAGACCAACGACTCTCTGTGAA 101
DB 42 |||||
QY 159 GAGCCTTGGGAGCAAGAGTGCAAGTGGTGTGCCACTGCTTCCCTGTGCGAGGGGAG 218
DB 102 GAGCCTTGGGAGCAAGAGTGCAAGTGGTGTGCCACTGCTTCCCTGTGCGAGGGGAG 161
QY 219 CGGCAAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGCGCTTCATGATCCCGAG 278
DB 162 CGGCAAGAGCAAGTGGTGGCTTGGGAGACTACGATGACAGCGCTTCATGATCCCGAG 221
QY 279 GTACCAAGTCCATGGAGAGATCTGGACAAAGCTCCACAGAGCTGCCTGTGGGGTAAAGT 338
DB 222 GTACCAAGTCCATGGAGAGATCTGGACAAAGCTCCACAGAGCTGCCTGTGGGGTAAAGT 281
QY 339 CCCGAGAAAGGATCTCATGCTCATGCTCAGGGAACATGATGTGAAAGAGGGAACAAGCA 398
DB 282 CCCGAGAAAGGATCTCATGCTCATGCTCAGGGAACATGATGTGAAAGAGGGAACAAGCA 341
QY 399 AAGAGAGCTGCTCTACATCTGGGCTCTGCCAATGGGAATTCAGAACTAGTAAACTCTGT 458
DB 342 AAGAGAGCTGCTCTACATCTGGGCTCTGCCAATGGGAATTCAGAACTAGTAAACTCTGT 401
QY 459 GCTGGACAGACGATGTCAAATTAATGTCTCTTGAACAACAAAGAGGACAGCTCTGACAA 518
DB 402 GCTGGACAGACGATGTCAAATTAATGTCTCTTGAACAACAAAGAGGACAGCTCTGACAA 461
QY 519 GGCCTGTACATGCCAGGAGATGATGTGCGTAAATGTTGTGGAACATGGCACTGATCC 578
DB 462 GGCCTGTACATGCCAGGAGATGATGTGCGTAAATGTTGTGGAACATGGCACTGATCC 521
QY 579 AAATATATCCAGATGAGTATGGAATATACCACTCTACATATGCTGTCTACATGAAGATAA 638
DB 522 AAATATATCCAGATGAGTATGGAATATACCACTCTACATATGCTGTCTACATGAAGATAA 581
QY 639 ATTAATGGCCAAAGCACTGCTCTTATAGGTGCTGATATGGAATCAAAAAACAGCATGG 698
DB 582 ATTAATGGCCAAAGCACTGCTCTTATAGGTGCTGATATGGAATCAAAAAACAGCATGG 641
QY 699 CCTCACACCACTGCTACTTGGTATACATGAGCAAAACAGCAAGTGTGAAATTTTAAAT 758
DB 642 CCTCACACCACTGCTACTTGGTATACATGAGCAAAACAGCAAGTGTGAAATTTTAAAT 701
QY 759 CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC 818
DB 702 CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC 761
QY 819 TGTATGTTGGATCAGCAAGTATAGTCAGCCCTTACTTGCAGCAAAATGTCATGATTC 878
DB 762 TGTATGTTGGATCAGCAAGTATAGTCAGCCCTTACTTGCAGCAAAATGTCATGATTC 821
QY 879 TTCTCAAGATCTGGAAGACGCGCAGAGATGATGCTGTTTCTAGTCATCATCATG 933

Db 822 TTCTCAAGATCTGGAAAGACGGCCAGAGATGCTGTTCTTAGTCAATCATG 876

RESULT 9
 LOCUS AX267557 879 bp DNA linear PAT 26-OCT-2001
 DEFINITION Sequence 531 from Patent WO0173032.
 ACCESSION AX267557
 VERSION AX267557.1 GI:16516281
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
 Kalos, M.D., Fanger, G.R., Renter, M.W., Stolk, D.A., Day, C.H.,
 Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T.
 and Henderson, R.A.
 TITL Composition and methods for the therapy and diagnosis of prostate
 cancer
 JOURNAL Patent: WO 0173032-A 531 04-OCT-2001;
 CORIXA CORPORATION (US)
 FEATURES
 source Location/Qualifiers
 1..879
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
 Query Match 78.6%; Score 733; DB 6; Length 879;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGCAAGAGCAACCTGGGCACCTCTGGAGACCAACGACCTCTCTGTGAA 158
 Db 42 CAGGGGAGCGGCAAGAGCAACCTGGGCACCTCTGGAGACCAACGACCTCTCTGTGAA 101

QY 159 GAGCTTTGGAGCAAGAGTGCAAGTGGTGTCTGCCACTGCTTCCCTGCTGCAGGGGGAG 218
 Db 102 GAGCTTTGGAGCAAGAGTGCAAGTGGTGTCTGCCACTGCTTCCCTGCTGCAGGGGGAG 161

QY 219 CGGCAAGAGCAACGTGGGCGCTTTGGGAGACTACGATGACAGCGCTTTCATGATCCAG 278
 Db 162 CGGCAAGAGCAACGTGGTGGTGGGAGACTACGATGACAGCGCTTTCATGATCCAG 221

QY 279 GTACCAGTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTCCCTGGTGGGTAAAGT 338
 Db 222 GTACCAGTCCATGGAGAAGATCTGACAGCTCCACAGAGCTCCCTGGTGGGTAAAGT 281

QY 339 CCCAGAAAGGATCTCATGCTGCTCAGGAGCACTGATGTGAACAAGAGGACAGCA 398
 Db 282 CCCAGAAAGGATCTCATGCTGCTCAGGAGCACTGATGTGAACAAGAGGACAGCA 341

QY 399 AAGAGAGCTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAACCTCGT 458
 Db 342 AAGAGAGCTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAACCTCGT 401

QY 459 GCTGGACAGACGATGTCACCTTAATGCTTTGACACAAACAAAGAGGACAGCTCTGACAAA 518
 Db 402 GCTGGACAGACGATGTCACCTTAATGCTTTGACACAAACAAAGAGGACAGCTCTGACAAA 461

QY 519 GGCCGTACATGCCAGGAAGATGAATGGTGGTAAATGCTGTGGAACAATGGCACTGATCC 578
 Db 462 GGCCGTACATGCCAGGAAGATGAATGGTGGTAAATGCTGTGGAACAATGGCACTGATCC 521

QY 579 AAATATTCCAGATGAGTATGGAAATACCACTACACTATGCTGTCTACATGAAGATAA 638
 Db 522 AAATATTCCAGATGAGTATGGAAATACCACTACACTATGCTGTCTACATGAAGATAA 581

QY 639 ATTAATGGCAAGCACTGCTCTTATACGCTGCTGATATCGAATCAAAACACAGCACTGG 698

Db 582 ATTAATGGCCAAAGCACTGCTCTTATACGGTGTCTGATATCGAATCAAAAAACAAGCATGG 641
Qy 699 CTTACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAAT 758
Db 642 CTTACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAAT 701
Qy 759 CAAGAAAAAAGCGAATTTAAATCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC 818
Db 702 CAAGAAAAAAGCGAATTTAAATCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC 761
Qy 819 TGTATGTTGGATCAGCAATGATAGTACAGCCCTCTACTTGACCAAAATGTTGATGATC 878
Db 762 TGTATGTTGGATCAGCAATGATAGTACAGCCCTCTACTTGACCAAAATGTTGATGATC 821
Qy 879 TTTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTCTTCTAGTCAATCATG 933
Db 822 TTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTCTTCTAGTCAATCATG 876

RESULT 10
AX316977
LOCUS AX316977 879 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 314 from Patent WO0190152.
ACCESSION AX316977
VERSION AX316977.1 GI:17900048
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Frudakis,T.N., Reed,S.G., Smith,J.M., Misher,L.E., Dillon,D.C.,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Retter,M.W., Wang,A., Skelky,Y.A., Harlocker,S.L. and Day,C.H.
Compositions and methods for the therapy and diagnosis of breast
JOURNAL cancer
PATENT: WO 0190152-A 314 29-NOV-2001;
CORIXA CORPORATION (US);
FEATURES
source Location/Qualifiers
1..879
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 78.6%; Score 733; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 99 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA 101
Qy 159 GACGCTTGGAGCAAGAGTGGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 218
Db 102 GACGCTTGGAGCAAGAGTGGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 161
Qy 219 CGGCAAGAGCAAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAG 278
Db 162 CGGCAAGAGCAAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAG 221
Qy 279 GTACCAAGTCCATGGAGAGATCTGGAGCAAGTCCAGAGCTGCTGGTGGGTTAAAGT 338
Db 222 GTACCAAGTCCATGGAGAGATCTGGAGCAAGTCCAGAGCTGCTGGTGGGTTAAAGT 281
Qy 339 CCCAGAAAGGATCTATCTGCTCAGGAGCACTGTGTAACAAAGAGGAGCAAGCA 398
Db 282 CCCAGAAAGGATCTATCTGCTCAGGAGCACTGTGTAACAAAGAGGAGCAAGCA 341
Qy 399 AAAGAGGACTGCTTACATCTGGCTCTGCAATGGGAATTCAGAAAGTAGTAAAGTCTGT 458
Db 342 AAAGAGGACTGCTTACATCTGGCTCTGCAATGGGAATTCAGAAAGTAGTAAAGTCTGT 401
Qy 459 GCTGGACAGAGATGTCAACTTATGCTTGTGACAAAGAGGAGCAAGTCTGTGACAAA 518

Db 402 GCTGGACAGACGATGTCACTTAATGCTTGTGACAAAGAGGAGCAAGTCTGTGACAAA 461
Qy 519 GGCCGTAACAATGCCAGGAAGATGATGTCGTTAATGTTGTTGTTGTTGTTGTTGTTGTT 578
Db 452 GGCCGTAACAATGCCAGGAAGATGATGTCGTTAATGTTGTTGTTGTTGTTGTTGTTGTT 521
Qy 579 AAATATTCAGATGATGATGGAATACCACTTACATGATGCTGTCTCAATGAAGATAA 638
Db 522 AAATATTCAGATGATGATGGAATACCACTTACATGATGCTGTCTCAATGAAGATAA 581
Qy 639 ATTAATGCCAAAGCACTGCTCTTATACGGTGGTGGATATCGAATCAAAAAACAAGCATGG 698
Db 582 ATTAATGCCAAAGCACTGCTCTTATACGGTGGTGGATATCGAATCAAAAAACAAGCATGG 641
Qy 699 CTTACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAAT 758
Db 642 CTTACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAAT 701
Qy 759 CAAGAAAAAAGCGAATTTAAATCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC 818
Db 702 CAAGAAAAAAGCGAATTTAAATCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC 761
Qy 819 TGTATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 878
Db 762 TGTATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 821
Qy 879 TTTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTCTTCTAGTCAATCATG 933
Db 822 TTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTCTTCTAGTCAATCATG 876

RESULT 11
AR261058
LOCUS AR261058 1852 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 530 from patent US 6321716.
ACCESSION AR261058
VERSION AR261058.1 GI:28071821
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1852)
AUTHORS Mashiki,Z. and Harada,J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: US 6321716-A 530 27-NOV-2001;
FEATURES
source Location/Qualifiers
1..1852
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 78.6%; Score 733; DB 6; Length 1852;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 99 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA 158
Db 771 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA 830
Qy 159 GACGCTTGGAGCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 218
Db 831 GACGCTTGGAGCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 890
Qy 219 CGGCAAGAGCAAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAG 278
Db 891 CGGCAAGAGCAAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAG 950
Qy 279 GTACCAAGTCCATGGAGAGATCTGGCAAGCTCCAGAGCTGCTGGTGGGTTAAAGT 338
Db 951 GTACCAAGTCCATGGAGAGATCTGGCAAGCTCCAGAGCTGCTGGTGGGTTAAAGT 1010
Qy 339 CCCAGAAAGGATCTCACTGCTGCTGAGGAGCACTGTGTAACAAAGAGGAGCAAGCA 398

RESULT 15
AR405588
LOCUS AR405588 1852 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 530 from patent US 6630305.
ACCESSION AR405588
VERSION AR405588.1 GI:40154425
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1852)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fager, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Sheiky, Y.A.W.,
Hepler, W.T., and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6630305-A 530 07-OCT-2003;
FEATURES Location/Qualifiers
source 1..1852
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 78.6%; Score 733; DB 6; Length 1852;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 99 CAGGGGAGCGGCAAGAGCAACGTGGGCACCTTTGGAGACCAACAGACCTCTCTGTGAA 158
Db 771 CAGGGGAGCGGCAAGAGCAACGTGGGCACCTTTGGAGACCAACAGACCTCTCTGTGAA 830

Qy 159 GACGCTTTGGGAGCAAGAGGTGCAAGTGGTGTGCTGCTCCCTGCTGCGAGGGGGAG 218
Db 831 GACGCTTTGGGAGCAAGAGGTGCAAGTGGTGTGCTGCTCCCTGCTGCGAGGGGGAG 890

Qy 219 CGGCAAGAGCAACGTGGCGCTTTGGGAGACTACGATGACAGCGCCCTTCATGGATCCCAG 278
Db 891 CGGCAAGAGCAACGTGGCGCTTTGGGAGACTACGATGACAGCGCCCTTCATGGATCCCAG 950

Qy 279 GTACGAGTCCATGGAGAGATCTGGACAGCTCCAGAGCTGCTGGTGGGGTAAAGT 338
Db 951 GTACGAGTCCATGGAGAGATCTGGACAGCTCCAGAGCTGCTGGTGGGGTAAAGT 1010

Qy 339 CCCAGAAAGGATCTCATGCTCAGGGACACTGTGAAACAAGAGGGACCAAGCA 398
Db 1011 CCCAGAAAGGATCTCATGCTCAGGGACACTGTGAAACAAGAGGGACCAAGCA 1070

Qy 399 AAGAGGACTGCTTACATCTGGCTCTGCCATGGGAATTCAGAGTAGTAAACTCGT 458
Db 1071 AAGAGGACTGCTTACATCTGGCTCTGCCATGGGAATTCAGAGTAGTAAACTCGT 1130

Qy 459 GCTGCAGACGAGTGTCAACTTAATGCTTGAACAACAAAAGAGGACAGCTCTGACAAA 518
Db 1131 GCTGCAGACGAGTGTCAACTTAATGCTTGAACAACAAAAGAGGACAGCTCTGACAAA 1190

Qy 519 GGCGGTACAATGCCAGGAAGTAAATGCGTTAATGTTGCGAACAATGGCACTATCC 578
Db 1191 GGCGGTACAATGCCAGGAAGTAAATGCGTTAATGTTGCGAACAATGGCACTATCC 1250

Qy 579 AAATATTCAGATGAGTAAATACCACTACACTATGCTGTACAAATGAAGATAA 638
Db 1251 AAATATTCAGATGAGTAAATACCACTACACTATGCTGTACAAATGAAGATAA 1310

Qy 639 ATTAATGCCAAAGCACTGCTTTATAGGCTGTGATATCGAATCAAAAAACAAGCATGG 698
Db 1311 ATTAATGCCAAAGCACTGCTTTATAGGCTGTGATATCGAATCAAAAAACAAGCATGG 1370

Qy 699 CCTCACACCACTGCTTGTGTATACATGACCAACAGCAAGTGGTGAATTTTAAAT 758
Db 1371 CCTCACACCACTGCTTGTGTATACATGACCAACAGCAAGTGGTGAATTTTAAAT 1430

Qy 759 CAGAAAAAGCGAATTTAAATGGCTGGATAGATGGAGAACTGCTCTCATCTTGC 818
Db 1431 CAGAAAAAGCGAATTTAAATGGCTGGATAGATGGAGAACTGCTCTCATCTTGC 1490

Qy 819 TGTATGTTTGGATCAGCAAGTATAGTCAGCCCTCTACTTTGAGCAAAATGTTGATGTATC 878
Db 1491 TGTATGTTTGGATCAGCAAGTATAGTCAGCCCTCTACTTTGAGCAAAATGTTGATGTATC 1550

Qy 879 TTCTCAAGATCTGAAAGACGGCCAGAGAGTATGCTGTTCTTAGTCATCATCATG 933
Db 1551 TTCTCAAGATCTGAAAGACGGCCAGAGAGTATGCTGTTCTTAGTCATCATCATG 1605

Search completed: April 30, 2004, 15:23:55
Job time : 3749 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 13:07:43 ; Search time 426 Seconds
(without alignments)
9304.152 Million cell updates/sec

Title: US-10-079-137B-343
Perfect score: 933
Sequence: 1 atggttggtgaggttgattc.....tggtttctagtcacatcatg 933

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N:Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	933	100.0	933	9	Adc15395 Human bre
2	835	89.5	876	9	Adc15394 Human bre
3	748	80.2	939	9	Adc15396 Human bre
4	733	78.6	876	9	Adc15393 Human bre
5	733	78.6	879	3	AAc81016 Human bre
6	733	78.6	879	4	AAH93826 Human pro
7	733	78.6	879	4	AAH93826 Human pro
8	733	78.6	879	4	AAH85140 Human pro
9	733	78.6	879	5	AAH59727 Prostate
10	733	78.6	879	6	ABl95290 Human B30
11	733	78.6	879	6	AAH93862 Breast tu
12	733	78.6	879	7	AAc95454 Prostate
13	733	78.6	879	7	Adc15393 Human bre
14	733	78.6	879	9	Adc15366 Human bre
15	733	78.6	879	9	Adc15396 Human pro
16	733	78.6	879	3	AAc81015 Human bre
17	733	78.6	879	3	AAH93825 Human pro
18	733	78.6	879	4	AAH93825 Human pro
19	733	78.6	879	4	AAH93825 Human pro
20	733	78.6	879	4	AAH85139 Human pro
21	733	78.6	879	5	AAH59726 Prostate
22	733	78.6	879	5	AAH59726 Prostate
23	733	78.6	879	6	AAH95289 Human B30
24	733	78.6	879	6	AAH95289 Human B30
25	733	78.6	879	6	AAH95289 Human B30
26	733	78.6	879	6	AAH95289 Human B30
27	733	78.6	879	6	AAH95289 Human B30
28	733	78.6	879	6	AAH95289 Human B30
29	733	78.6	879	6	AAH95289 Human B30
30	733	78.6	879	6	AAH95289 Human B30
31	733	78.6	879	6	AAH95289 Human B30
32	733	78.6	879	6	AAH95289 Human B30
33	733	78.6	879	6	AAH95289 Human B30
34	733	78.6	879	6	AAH95289 Human B30
35	733	78.6	879	6	AAH95289 Human B30
36	733	78.6	879	6	AAH95289 Human B30
37	733	78.6	879	6	AAH95289 Human B30
38	733	78.6	879	6	AAH95289 Human B30
39	733	78.6	879	6	AAH95289 Human B30
40	733	78.6	879	6	AAH95289 Human B30
41	733	78.6	879	6	AAH95289 Human B30
42	733	78.6	879	6	AAH95289 Human B30
43	733	78.6	879	6	AAH95289 Human B30
44	733	78.6	879	6	AAH95289 Human B30
45	733	78.6	879	6	AAH95289 Human B30

ALIGNMENTS

RESULT 1

ADc15395	78.6	1852	7	ACC95453	Prostate	
ID ADc15395 standard; DNA; 933 BP.	78.6	1852	7	ADa11392	Human bre	
XX	733	78.6	1852	9	ADc15365	Human bre
AC ADc15395;	733	78.6	1852	9	ADb13980	Human pro
DT 18-DEC-2003 (first entry)	733	78.6	1852	9	ADb13980	Human pro
XX	733	78.6	1852	9	ADb13980	Human pro
DE Human breast tumour protein DNA, SEQ ID 343.	733	78.6	1852	9	ADb13980	Human pro
XX	733	78.6	1852	9	ADb13980	Human pro
KW Cytostatic; Gene therapy; breast cancer; breast tumour protein; human; ds.	733	78.6	1852	9	ADb13980	Human pro
XX	733	78.6	1852	9	ADb13980	Human pro
OS Homo sapiens.	733	78.6	1852	9	ADb13980	Human pro
XX	733	78.6	1852	9	ADb13980	Human pro
PN WO2003013431-A2.	733	78.6	1852	9	ADb13980	Human pro
XX	733	78.6	1852	9	ADb13980	Human pro
PD 20-FEB-2003.	733	78.6	1852	9	ADb13980	Human pro
XX	733	78.6	1852	9	ADb13980	Human pro
PF 05-AUG-2002; 2002WO-US024917.	733	78.6	1852	9	ADb13980	Human pro
XX	733	78.6	1852	9	ADb13980	Human pro
PR 07-AUG-2001; 2001US-00924400.	733	78.6	1852	9	ADb13980	Human pro
PR 20-FEB-2002; 2002US-00079137.	733	78.6	1852	9	ADb13980	Human pro
PR 02-AUG-2002; 2002US-00212679.	733	78.6	1852	9	ADb13980	Human pro
(CORI-) CORIXA CORP.	733	78.6	1852	9	ADb13980	Human pro
Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH; Kalos MD;	733	78.6	1852	9	ADb13980	Human pro
WPI; 2003-342398/32.	733	78.6	1852	9	ADb13980	Human pro
New polynucleotide, useful for preparing a composition for diagnosing, treating or preventing cancer.	733	78.6	1852	9	ADb13980	Human pro
Claim 1; SEQ ID NO 343; 308pp; English.	733	78.6	1852	9	ADb13980	Human pro

The present invention relates to compositions and methods for the therapy and diagnosis of cancer, particularly breast cancer. The method for detecting the presence of a cancer in a patient comprises: obtaining a biological sample from the patient; contacting the biological sample with a binding agent that binds to the polypeptide; detecting in the sample an amount of the polypeptide that binds to the binding agent; and comparing the amount of the polypeptide to a predetermined cut-off value. Treating breast cancer comprises administering a composition comprising breast tumour proteins and nucleic acids, which simulates and/or expands T cells

CC specific for the tumour protein. The present sequence was used to
CC illustrate the invention.
XX

SQ Sequence 933 BP; 272 A; 201 C; 248 G; 212 T; 0 U; 0 Other;
Query Match 100.0%; Score 933; DB 9; Length 933;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 933; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGGTTCAGGTTGATTCATGCGCGCTGCTCTCTGTGAAGAGCAATTTGGTCTC 60
Db 1 ATGGTGGTTCAGGTTGATTCATGCGCGCTGCTCTCTGTGAAGAGCAATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTCTGCTCTCTCTGTCAGGGGAGCGGCAAGAGCAAC 120
Db 61 AGGAGCAAGATGGGCAAGTGGTCTGCTCTCTCTGTCAGGGGAGCGGCAAGAGCAAC 120
QY 121 GTGGGCACTTCTGGACACCAACAGCACTCTCTGTGAAGACGCTTGGGAGCAAGAGTGC 180
Db 121 GTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAAGACGCTTGGGAGCAAGAGTGC 180
QY 181 AAGTGTGTGTCACCTGCTTCCCTGCTCAGGGGAGCGGCAAGCAACCTGGGCGCT 240
Db 181 AAGTGTGTGTCACCTGCTTCCCTGCTCAGGGGAGCGGCAAGCAACCTGGGCGCT 240
QY 241 TGGGGAGACTACGATCACAGCGCTTCATGGATCCAGGTACACGTCCTCATGGAGAAGAT 300
Db 241 TGGGGAGACTACGATCACAGCGCTTCATGGATCCAGGTACACGTCCTCATGGAGAAGAT 300
QY 301 CTGCAAGGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAGAAAGGATCTCATCTG 360
Db 301 CTGCAAGGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAGAAAGGATCTCATCTG 360
QY 361 ATGCTCAGGAGCACTATGTGACAGAGGCGCAAGCAAGAGCACTGCTTACATCTG 420
Db 361 ATGCTCAGGAGCACTATGTGACAGAGGCGCAAGCAAGAGCACTGCTTACATCTG 420
QY 421 GCCTCTGCCAATGGGAATTCAGAAGTAGTAAACTCGTCTGACAGAGCATGTCACTT 480
Db 421 GCCTCTGCCAATGGGAATTCAGAAGTAGTAAACTCGTCTGACAGAGCATGTCACTT 480
QY 481 AATGCTCTTGACAAACAAAGAGGAGCAGCTCTGCAAGGCGGTACATGCCAGGAAGAT 540
Db 481 AATGCTCTTGACAAACAAAGAGGAGCAGCTCTGCAAGGCGGTACATGCCAGGAAGAT 540
QY 541 GAATGTGCGTTAATGTGTGGAACATGCACTGATCCAAATATTCAGATCAGTATGA 600
Db 541 GAATGTGCGTTAATGTGTGGAACATGCACTGATCCAAATATTCAGATCAGTATGA 600
QY 601 AATACCACTCTACATATGCTGTCTCAATGAAGATAAATTAATGCCAAAGCACTGCTC 660
Db 601 AATACCACTCTACATATGCTGTCTCAATGAAGATAAATTAATGCCAAAGCACTGCTC 660
QY 661 TTATACGGTCTGATATCGAATCAAAAAAAGCATGGCTCACACCACTGCTACTTGT 720
Db 661 TTATACGGTCTGATATCGAATCAAAAAAAGCATGGCTCACACCACTGCTACTTGT 720
QY 721 ATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAAGCGAATTAAT 780
Db 721 ATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAAGCGAATTAAT 780
QY 781 GCCTGGATAGATATGGAGAACTGCTCTCATCTTGTATGTTGTTGATCAGCAAGT 840
Db 781 GCCTGGATAGATATGGAGAACTGCTCTCATCTTGTATGTTGTTGATCAGCAAGT 840
QY 841 ATAGTCAGCCCTCTACTTGGAGCAAAATGTTGATGATCTTCTCAAGATCTGGAAGAGCG 900
Db 841 ATAGTCAGCCCTCTACTTGGAGCAAAATGTTGATGATCTTCTCAAGATCTGGAAGAGCG 900
QY 901 CCAGAGATATGCTGTTTCTAGTCATCATG 933
Db 901 CCAGAGATATGCTGTTTCTAGTCATCATG 933

RESULT 2

ADCL5394
XX ADCL5394 standard; DNA; 876 BP.
AC ADCL5394;
XX ADCL5394;
DT 18-DEC-2003 (first entry)
XX Human breast tumour protein DNA, SEQ ID 342.
XX Cytostatic; Gene therapy; breast cancer; breast tumour protein; human;
XX ds.
XX Homo sapiens.
OS WO2003013431-A2.
XX 20-FEB-2003.
XX 05-AUG-2002; 2002WO-US024917.
XX 07-AUG-2001; 2001US-00924400.
XX 20-FEB-2002; 2002US-00079137.
XX 02-AUG-2002; 2002US-00212679.
XX (CORI-) CORIXA CORP.
XX Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;
PI Kalos MD;
XX WPI; 2003-342398/32.
XX New polynucleotide, useful for preparing a composition for diagnosing,
XX treating or preventing cancer.
PS Claim 1; SEQ ID NO 342; 308pp; English.
XX The present invention relates to compositions and methods for the therapy
XX and diagnosis of cancer, particularly breast cancer. The method for
XX detecting the presence of a cancer in a patient comprises: obtaining a
XX biological sample from the patient; contacting the biological sample with
XX a binding agent that binds to the polypeptide; detecting in the sample an
XX amount of the polypeptide that binds to the binding agent; and comparing
XX the amount of the polypeptide to a predetermined cut-off value. Treating
XX breast cancer comprises administering a composition comprising breast
XX tumour proteins and nucleic acids, which simulates and/or expands T cells
XX specific for the tumour protein. The present sequence was used to
XX illustrate the invention.
SQ Sequence 876 BP; 261 A; 193 C; 222 G; 200 T; 0 U; 0 Other;
Query Match 89.5%; Score 835; DB 9; Length 876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 835; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 99 CAGGGGAGCGGCAAGAGCAACGTGGCACTTCTGAGACCAACAGCACTCTCTGTGAA 159
Db 42 CAGGGGAGCGGCAAGAGCAACGTGGCACTTCTGAGACCAACAGCACTCTCTGTGAA 101
QY 159 GAGCCTTTGGGAGCAAGAGGTGCAAGTGTCTGCTGCTCTCCCTGCTGAGGGGAG 218
Db 102 GAGCCTTTGGGAGCAAGAGGTGCAAGTGTCTGCTGCTCTCCCTGCTGAGGGGAG 161
QY 219 CGGCAAGAGCAACGTGGGCGCTTTGGGAGACTACGATGACAGCGCTTCATGATCCAG 278
Db 162 CGGCAAGAGCAACGTGGGCGCTTTGGGAGACTACGATGACAGCGCTTCATGATCCAG 221
QY 279 GTACCAAGTCCATGGAGAAAGATCTGACAGCTCCACAGAGCTGCTGTTGGGTAAGT 338
Db 222 GTACCAAGTCCATGGAGAAAGATCTGACAGCTCCACAGAGCTGCTGTTGGGTAAGT 281
QY 339 CCCAGAAAGATCTCATCTGCTCAGGGACACTGTATGTGAAACAGAGGGGCAAGCA 398

Db 282 CCCAGAGAGGATCTCATGCTCATGCTCAGGACACTGATGTGACAAAGAGGACACAGCA 341
Qy 399 AAAGAGAGCTCTCTACATCTGGGCTCTGCAATGGGAATTCAGAGTAGTAAACTCGT 458
Db 342 AAAGAGAGCTCTCTACATCTGGGCTCTGCAATGGGAATTCAGAGTAGTAAACTCGT 401
Qy 459 GCTGACAGAGCTCTCAACTTAATGCTTGTGACACAAAGAGAGGACAGCTCTGACAAA 518
Db 402 GCTGACAGAGCTCTCAACTTAATGCTTGTGACACAAAGAGAGGACAGCTCTGACAAA 461
Qy 519 GGCGCTCAATGCCAGGAAGTGAATGCGTTAATGTTGCGAATGCAATGCAATGCAATG 578
Db 462 GGCGCTCAATGCCAGGAAGTGAATGCGTTAATGTTGCGAATGCAATGCAATGCAATG 521
Qy 579 AAATATTCACAGATGATGGAATACACCTCTACACTATGCTCTCTACATGAGATAA 638
Db 522 AAATATTCACAGATGATGGAATACACCTCTACACTATGCTCTCTACATGAGATAA 581
Qy 639 ATTAATGGCCAAAGCACTGCTTTATACGGTGTGATATGCAATCAAAAAACAGCATGG 698
Db 582 ATTAATGGCCAAAGCACTGCTTTATACGGTGTGATATGCAATCAAAAAACAGCATGG 641
Qy 699 CCTCACACCTGCTACTTGTGATACATGACCAAAACAGCAAGTGTGAAATTTTAAT 758
Db 642 CCTCACACCTGCTACTTGTGATACATGACCAAAACAGCAAGTGTGAAATTTTAAT 701
Qy 759 CAAGAAAAGCGAATTTAAATGCGCTGATATGGAAGAACTGCTCTCATCTTGC 818
Db 702 CAAGAAAAGCGAATTTAAATGCGCTGATATGGAAGAACTGCTCTCATCTTGC 761
Qy 819 TGTATGTTGTGGATCAGCAATATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGATC 878
Db 762 TGTATGTTGTGGATCAGCAATATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGATC 821
Qy 879 TTCTCAAGATCTGGAAGACGCGCAGAGATGCTGTTTCTAGTCATCATG 933
Db 822 TTCTCAAGATCTGGAAGACGCGCAGAGATGCTGTTTCTAGTCATCATG 876

RESULT 3

ADCL15396
ID ADCL15396 standard; DNA; 939 BP.
XX AC ADCL15396;
XX AC ADCL15396;
DT 18-DEC-2003 (first entry)
DE Human breast tumour protein DNA, SEQ ID 344.

XX Human breast tumour protein DNA, SEQ ID 344.
KW Cytostatic; Gene therapy; breast cancer; breast tumour protein; human;
ds.

XX Homo sapiens.

XX WO2003013431-A2.

XX 20-FEB-2003.

XX 05-AUG-2002; 2002WO-US024917.

XX 07-AUG-2001; 2001US-00924400.

XX 20-FEB-2002; 2002US-00079137.

XX 02-AUG-2002; 2002US-00212679.

XX (CORI-) CORIXA CORP.

XX Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;

XX Kalos MD;

XX WPI; 2003-342398/32.

XX New polynucleotide, useful for preparing a composition for diagnosing,

PT treating or preventing cancer.

XX Claim 1; SEQ ID NO 344; 308pp; English.

XX The present invention relates to compositions and methods for the therapy
CC and diagnosis of cancer, particularly breast cancer. The method for
CC detecting the presence of a cancer in a patient comprises: obtaining a
CC biological sample from the patient; contacting the biological sample with
CC a binding agent that binds to the polypeptide; detecting in the sample an
CC amount of the polypeptide that binds to the binding agent; and comparing
CC the amount of the polypeptide to a predetermined cut-off value. Treating
CC breast cancer comprises administering a composition comprising breast
CC tumour proteins and nucleic acids, which simulates and/or expands T cells
CC specific for the tumour protein. The present sequence was used to
CC illustrate the invention.

XX Sequence 939 BP; 273 A; 204 C; 249 G; 213 T; 0 U; 0 Other;

Query Match 80.2%; Score 748; DB 9; Length 939;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 848; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 84 CTGCTTTCCCTGCTCAGGGGAGCGGCAAGAGCAACGTGGGCACCTTCGGAGACCACAA 143

Db 90 CTGCTTTCCCTGCTCAGGGGAGCGGCAAGAGCAACGTGGGCACCTTCGGAGACCACAA 149

Qy 144 CGACTCTCTGTGAAGACGCTTTGGGAGCAAGAGGTGCAAGTGGTGGTCCACTGTCTCC 203

Db 150 CGACTCTCTGTGAAGACGCTTTGGGAGCAAGAGGTGCAAGTGGTGGTCCACTGTCTCC 209

Qy 204 CTGCTCAGGGGAGCGGCAAGAGCAACGTGGGCCTTGGGAGACTAGATGACAGCGC 263

Db 210 CTGCTCAGGGGAGCGGCAAGAGCAACGTGGGCCTTGGGAGACTAGATGACAGCGC 269

Qy 264 CTTATGATGCCAGGTACACGCTCCATGGAAGATCTGGAAGAGCTCCACAGAGCTGC 323

Db 270 CTTATGATGCCAGGTACACGCTCCATGGAAGATCTGGAAGAGCTCCACAGAGCTGC 329

Qy 324 CTGCTGGGTTAAAGTCCCGAAGAGATCTCATCTGCTCAGGACACTGATGTGAA 383

Db 330 CTGCTGGGTTAAAGTCCCGAAGAGATCTCATCTGCTCAGGACACTGATGTGAA 389

Qy 384 CAAGAGGCAAGCAAGAGAGAGCTCTCATCTGCTGCTTGGCCTTGGCAATGGAATTCAGA 443

Db 390 CAAGAGGCAAGCAAGAGAGAGCTCTCATCTGCTGCTTGGCCTTGGCAATGGAATTCAGA 449

Qy 444 AGTAGTAAACTCGTCTGACAGAGATGTCAACTTAATGTCCTTGAACAACAAAGAG 503

Db 450 AGTAGTAAACTCGTCTGACAGAGATGTCAACTTAATGTCCTTGAACAACAAAGAG 509

Qy 504 GACAGCTCTGACAAAGCGGCTACATGCCAGAGAGATGTCGTTAATGTTGCTGGA 563

Db 510 GACAGCTCTGACAAAGCGGCTACATGCCAGAGAGATGTCGTTAATGTTGCTGGA 569

Qy 564 ACATGGCACTGATCCAAATATTTCCAGATGATATGGAATACCACTCTACATGCTGT 623

Db 570 ACATGGCACTGATCCAAATATTTCCAGATGATATGGAATACCACTCTACATGCTGT 629

Qy 624 CTRCAATGAGATTAATTAATGCGCAAGCACTGCTCTTATACGGTGTGATATCGAATC 683

Db 630 CTRCAATGAGATTAATTAATGCGCAAGCACTGCTCTTATACGGTGTGATATCGAATC 689

Qy 684 AAAAAACAAGCATGGCCTCACACCACTGCTACTTGTATACATGAGCAAAAAACAGCAAGT 743

Db 690 AAAAAACAAGCATGGCCTCACACCACTGCTACTTGTATACATGAGCAAAAAACAGCAAGT 749

Qy 744 GGTGAATTTTAAATCAAGAAAACCGAATTTAAATGCGCTGATATGAGATATGGAAGAC 803

Db 750 GGTGAATTTTAAATCAAGAAAACCGAATTTAAATGCGCTGATATGAGATATGGAAGAC 809

Qy 804 TGCTCTCATCTTGTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 863

Db 810 TGCTCTCATCTTGTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 869

QY 864 AAATGTTGATGATCTTCTCAAGATCTGAAAGACGGCCAGAGAGATGCTGTTCTAGT 923
DB |||||
870 AAATGTTGATGATCTTCTCAAGATCTGAAAGACGGCCAGAGAGATGCTGTTCTAGT 929
QY 924 CATCATCATG 933
DB |||||
930 CATCATCATG 939

RESULT 4
ADCL15393
ID ADC15393 standard; DNA; 876 BP.
AC ADC15393;
XX
DT 18-DEC-2003 (first entry)
DE Human breast tumour protein DNA, SEQ ID 341.
XX
KW Cytostatic; Gene therapy; breast cancer; breast tumour protein; human;
KW ds.
XX
OS Homo sapiens.
XX
PN W02003013431-A2.
XX
PD 20-FEB-2003.
XX
PF 05-AUG-2002; 2002WO-US024917.
XX
PR 07-AUG-2001; 2001US-00924400.
PR 20-FEB-2002; 2002US-00079137.
PR 02-AUG-2002; 2002US-00212679.
XX
XX
PA (CORI-) CORIXA CORP.
XX
PI Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;
PI Kalos MD;
XX
DR WPI; 2003-342398/32.
XX
XX
PT New polynucleotide, useful for preparing a composition for diagnosing,
PT treating or preventing cancer.
XX
PS Claim 1; SEQ ID NO 341; 308pp; English.
XX
CC The present invention relates to compositions and methods for the therapy
CC and diagnosis of cancer, particularly breast cancer. The method for
CC detecting the presence of a cancer in a patient comprises: obtaining a
CC biological sample from the patient; contacting the biological sample with
CC a binding agent that binds to the polypeptide; detecting in the sample an
CC amount of the polypeptide that binds to the binding agent; and comparing
CC the amount of the polypeptide to a predetermined cut-off value. Treating
CC breast cancer comprises administering a composition comprising breast
CC tumour proteins and nucleic acids, which simulates and/or expands T cells
CC specific for the tumour protein. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 876 BP; 261 A; 193 C; 222 G; 200 T; 0 U; 0 Other;

Query Match 78.8%; Score 733; DB 9; Length 876;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGGAGCGGCAAGACCAAGCTGGGCGACTTCTGGAGACCAACAGACTCTCTGTGAA 158
DB |||||
42 CAGGGGGAGCGGCAAGACCAAGCTGGGCGACTTCTGGAGACCAACAGACTCTCTGTGNA 101
QY 159 GAGCCTTGGGAGCAAGAGGTGCAAGTGGTGGCTGCCACTGCTCCCTGCTGCAGGGGAG 218
DB |||||
102 GAGCCTTGGGAGCAAGAGGTGCAAGTGGTGGCTGCCACTGCTCCCTGCTGCAGGGGAG 161

QY 219 CGGCAAGAGCAACGTGGGCGCTTGGGAGAGACTACGATGACAGCGCCCTCATGATCCAG 278
DB |||||
162 CGGCAAGAGCAACGTGGTGGCTTGGGAGAGACTACGATGACAGCGCCCTCATGATCCAG 221
QY 279 GTACCAAGTCCATGGAGAGATCTGGAAGAAGCTCCAGAGCTCCAGAGCTGCTGGTGGGTAAGT 338
DB |||||
222 GTACCAAGTCCATGGAGAGATCTGGAAGAAGCTCCAGAGCTCCAGAGCTGCTGGTGGGTAAGT 281
QY 339 CCCAGAAAGGATCTCATGCTCATGCTCAGGGACACCTGATGTGAACAGAGGGGCAAGCA 398
DB |||||
282 CCCAGAAAGGATCTCATGCTCATGCTCAGGGACACCGATGTGAACAGAGGGGCAAGCA 341
QY 399 AAGAGAGCTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAACTCGT 458
DB |||||
342 AAGAGAGCTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAACTCGT 401
QY 459 GCTGGACAGAGATGTCAACTTAAATGCTTGAACAAACAAAGAGGAGCAGCTCTGCAAAA 518
DB |||||
402 GCTGGACAGAGATGTCAACTTAAATGCTTGAACAAACAAAGAGGAGCAGCTCTGCAAAA 461
QY 519 GGCGGTACAATGGCAGGAAGATGAATGTGGTAAATTTGCTGGAAACATGGCACTGATCC 578
DB |||||
462 GGCGGTACAATGGCAGGAAGATGAATGTGGTAAATTTGCTGGAAACATGGCACTGATCC 521
QY 579 AATATTCCAGATGAGTATGGAATACCACTCTACACTATGCTGTACAAATGAAGATAA 638
DB |||||
522 AATATTCCAGATGAGTATGGAATACCACTCTACACTATGCTGTACAAATGAAGATAA 581
QY 639 ATTAATGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAACAGCAATGG 698
DB |||||
582 ATTAATGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAACAGCAATGG 641
QY 699 CCTCACACCACTGCTCTGTTATACATGACGCAAAAACAGCAATGGTGAATTTTAAAT 758
DB |||||
642 CCTCACACCACTGCTCTGTTATACATGACGCAAAAACAGCAATGGTGAATTTTAAAT 701
QY 759 CAAGAAAAAGCGAATTTAAATGCGTGGTAGATATGGAAGAACTGCTCTCATCTATTC 818
DB |||||
702 CAAGAAAAAGCGAATTTAAATGCGTGGTAGATATGGAAGAACTGCTCTCATCTATTC 761
QY 819 TGTATGTTGGATCAGCAAGTATAGTCAGCCCTCTACTTTGAGCAAAATGTTGATGTATC 878
DB |||||
762 TGTATGTTGGATCAGCAAGTATAGTCAGCCCTCTACTTTGAGCAAAATGTTGATGTATC 821
QY 879 TTCTCAAGATCTGGAAGACGGCCAGAGAGTAGTGTCTTTCTAGTCTATCATCATG 933
DB |||||
822 TTCTCAAGATCTGGAAGACGGCCAGAGAGTAGTGTCTTTCTAGTCTATCATCATG 876

RESULT 5
AAC81016
ID AAC81016 standard; cDNA; 879 BP.
XX
AC AAC81016;
XX
DT 13-FEB-2001 (first entry)
DE Human breast tumour-specific antigen cDNA SEQ ID NO: 314.
XX
KW Human; breast tumour-specific antigen; cytostatic; vaccine;
KW breast cancer; B18Agl; B11Agl; B15Agl; ss.
OS Homo sapiens.
XX
PN W0200061753-A2.
XX
PD 19-OCT-2000.
XX
PF 07-APR-2000; 2000WO-US009312.
XX
PR 09-APR-1999; 99US-00289198.
PR 28-OCT-1999; 99US-00429755.
PR 23-MAR-2000; 2000US-00534825.

Qy	699	CCTCACCACTGCTACTTGGTATACATGACGAAAAACAGCAAGTGGTGAATTTTTTAAT	751		
Db	642	CCTCACCACTGCTACTTGGTATACATGACGAAAAACAGCAAGTGGTGAATTTTTTAAT	701		
Qy	759	CAAGAAAAAGCGAATTTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC	818		
Db	702	CAAGAAAAAGCGAATTTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC	761		
Qy	819	TGTATGTTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGGACAAAATGTTGATGTATC	878		
Db	762	TGTATGTTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGGACAAAATGTTGATGTATC	821		
Qy	879	TTCTCAAGATCTGGAAAGACGGCCAGAGAGATAGCTGTTTCTAGTCATCATCATG	933		
Db	822	TTCTCAAGATCTGGAAAGACGGCCAGAGAGATAGCTGTTTCTAGTCATCATCATG	876		
RESULT 6					
AAH93826	ID AAH93826 standard; cDNA; 879 BP.				
XX	AAH93826;				
DT	04-OCT-2001	(first entry)			
XX	Human prostate-specific cDNA sequence splice variant open reading frame.				
DE	Human; prostate cancer; prostate-specific; diagnosis; vaccine;				
XX	cytostatic; gene therapy; metastasis; ss.				
KW	Homo sapiens.				
OS	WO200151633-A2.				
XX	19-JUL-2001.				
XX	16-JAN-2001; 2001WO-US001574.				
XX	14-JAN-2000; 2000US-00483672.				
PR	(CORI-) CORIXA CORP.				
PA	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;				
XX	Kalsoe MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAM;				
PI	Wang A, Meagher MJ;				
XX	WPI; 2001-425873/45.				
DR	New polynucleotide encoding a prostate-specific protein, for diagnosing,				
XX	monitoring and treating prostate cancer in a patient and for use in				
PT	vaccines.				
XX	Claim 1; Page 408; 543pp; English.				
PS	The present invention describes polynucleotide sequences (I) which encode				
XX	prostate-specific proteins (II). (I) and (II) have cytostatic activity,				
CC	and can be used in vaccine production and gene therapy. (I), (II),				
CC	antibodies to (II), fusion proteins comprising (II), and isolated T cells				
CC	prepared using (I) or (II) are used treat cancer in a patient. (I) and				
CC	the antibodies are also used in the detection of cancer in a patient. (I)				
CC	cancer that is diagnosed or treated is particularly prostate cancer. (I)				
CC	and (II) can be used in vaccines. The antibodies or (I) can be used for				
CC	monitoring the progression of cancer in a patient. (I) and (II) can also				
CC	be used to improve diagnostic and therapeutic methods for prostate				
CC	cancer. They can indicate the level of metastasis as well as the prostate				
CC	volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent				
CC	polynucleotide and amino acid sequences used in the exemplification of				
CC	the present invention				
XX	Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;				
SQ					

Query Match 78.6%; Score 733; DB 4; Length 879;

Best Local Similarity 99.8%; Pred. No. 0;

Db 342 AAGAGGACTGCTCTACATCTGGGCTCTGGCAATGGGAATTCAGAAGTAGTAAACTCGT 401
QY 459 GCTGACAGACGATGTCAACTTAATGTCTTTGACACAAAAAGAGGACAGCTCTGCAAAA 518
Db 402 GCTGACAGACGATGTCAACTTAATGTCTTTGACACAAAAAGAGGACAGCTCTGCAAAA 461
QY 519 GGCGTCAATGCCAGGAAGATGAATGCGCTTAATGTCTTGAACATGGCACTGATCC 578
Db 462 GGCGTCAATGCCAGGAAGATGAATGCGCTTAATGTCTTGAACATGGCACTGATCC 521
QY 579 AAATATTCAGATGAGTAAATACCACTCTACACTATGCTCTCTACAATGAAGATAA 638
Db 522 AAATATTCAGATGAGTAAATACCACTCTACACTATGCTCTCTACAATGAAGATAA 581
QY 639 ATTAATGCCAAAGCACTGCTTTATACGGTGTGATATCGAATCAAAAAACAGCATGG 698
Db 582 ATTAATGCCAAAGCACTGCTTTATACGGTGTGATATCGAATCAAAAAACAGCATGG 641
QY 699 CCTCACCACTGCTACTTGTGTATACATGACAAAAACAGCAAGTGGTAAATTTTAAAT 758
Db 642 CCTCACCACTGCTACTTGTGTATACATGACAAAAACAGCAAGTGGTAAATTTTAAAT 701
QY 759 CAAGAAAAAGCGAATTTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATATTCG 818
Db 702 CAAGAAAAAGCGAATTTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATATTCG 761
QY 819 TGTATGTTGTGATCAGCAAGTATAGTCAGCCCTCTACTTGGACAAAAATGTTGATGATC 878
Db 762 TGTATGTTGTGATCAGCAAGTATAGTCAGCCCTCTACTTGGACAAAAATGTTGATGATC 821
QY 879 TTCTCAAGATCTGAAAGACGGCCAGAGAGATGCTGTTTCTAGTCATCATG 933
Db 822 TTCTCAAGATCTGAAAGACGGCCAGAGAGATGCTGTTTCTAGTCATCATG 876

RESULT 8

AAH85140

ID AAH85140 standard; cDNA; 879 BP.

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

Human prostate-specific sequence related cDNA sequence.

Human; prostate cancer; therapy; diagnosis; cat eye syndrome; chromosome 22q11.2; prostate-specific protein; chromosome 1; prostate specific antigen; PSA; ss.

Homo sapiens.

WO200134802-A2.

17-MAY-2001.

09-NOV-2000; 2000WO-US030904.

12-NOV-1999; 99US-00439313.

18-NOV-1999; 99US-00443686.

(CORI-) CORIXA CORP.

Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG; Kalos MD, Retter MW, Stoik JA, Day CH, Skeiky YAW, Wang A;

WPI; 2001-308785/32.

Isolated polypeptide comprising at least an immunogenic portion of a prostate-specific protein, useful in the diagnosis and therapy of prostate cancer.

Claim 5; Page 308; 325pp; English.

Db 822 TTCTCAGATCTGGAAGACGGCAGAGAGTATGCTGTTCTAGTCATCATCATG 876

RESULT 9

ACA59727

ID ACA59727 standard; cDNA; 879 BP.

AC ACA59727;

XX

DT 10-JUN-2003 (first entry)

XX

DE Prostate cancer therapy associated cDNA #464.

XX

KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;

KW immunogen; cancer; prostate specific antigen; PSA;

KW Prostatic acid phosphatase; PAP; prostate specific membrane antigen;

KW PSMA; gene; ss.

XX

OS Homo sapiens.

XX

PN US2002192763-A1.

XX

PD 19-DEC-2002.

XX

PF 29-JUN-2001; 2001US-00895793.

XX

PR 04-OCT-1999; 99US-0157455P.

PR

PR 04-OCT-2000; 2000US-00679272.

PR

PR 28-MAR-2001; 2001US-00822827.

XX

PA (XUJJ/) XU J.

PA (DILL/) DILLON D C.

PA (MITC/) MITCHAM J L.

PA (HARL/) HARLOCKER S L.

PA (JIAN/) JIANG Y.

PA (KALO/) KALOS M D.

PA (FANG/) FANGER G R.

PA (RETT/) RETTER M W.

PA (STOL/) STOLK J A.

PA (DAYC/) DAY C H.

PA (VEDV/) VEDVICK T S.

PA (CART/) CARTER D.

PA (LISX/) LI S X.

PA (WANG/) WANG A.

PA (SKEI/) SKEIKY Y A W.

PA (HEPL/) HEPLER W T.

PA (HEND/) HENDERSON R A.

PA (HURA/) HURAL J.

PA (MCNE/) MCNEILL P D.

PA (HOUG/) HOUGHTON R L.

PA (DRAS/) Y DE BASSOLS C V.

PA (FOYT/) FOY T M.

XX

Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS,

PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA,

PI McNeill PD, Houghton RL, Y De Bassols CV, Foy TM;

XX WPI; 2001-245062/25.

DR

XX

PT Prostate specific protein and its encoding polynucleotide, useful for the

PT treatment and diagnosis of prostate cancer.

XX

Example 11; SEQ ID NO 531; 85pp; English.

XX

CC The invention describes a fusion protein comprising at least one amino

CC acid sequence of immunogenic portions of any of the 3 sequences not

CC defined in the specification, or sequences having at least 70 or 90 %

CC sequence identity to any one of the 35 sequences defined in the USPTO web

CC site, which is encoded by any of the 4 nucleotide sequences not defined

CC in the specification. The fusion protein, composition and methods are

CC useful for diagnosing, preventing and/or treating cancer, particularly

CC prostate cancer. The proteins are useful as markers to indicate the

CC

CC presence or absence of cancer. This sequence represents a prostate cancer

CC therapy associated cDNA. Note: The sequence data for this patent did not

CC form part of the printed specification, but was obtained in electronic

CC format directly from the US patent office at

CC seqdata.uspto.gov/sequence.html?DocID=US20020192763

XX

SQ Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;

XX

Query Match 78.6%; Score 733; DB 5; Length 879;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGGAGCGGCAAGAGCAAGCTGGGCGACCTTCTGGAGACCACACGACTCTCTGTGAA 158

Db 42 CAGGGGGAGCGGCAAGAGCAAGCTGGGCGACCTTCTGGAGACCACACGACTCTCTGTGAA 101

QY 159 GACGCTTGGGAGCAAGAGGTGCAAGTGGTGTGCTGCCACTGCTTCCCTGCTGAGGGGAG 218

Db 102 GACGCTTGGGAGCAAGAGGTGCAAGTGGTGTGCTGCCACTGCTTCCCTGCTGAGGGGAG 161

QY 219 CGGCAAGAGCAAGCTGGGCGCTTGGGAGACTACGATGACAGCGCTTCTGATGCCAG 278

Db 162 CGGCAAGAGCAAGCTGGGCGCTTGGGAGACTACGATGACAGCGCTTCTGATGCCAG 221

QY 279 GTACCACGTCATGAGAGAGATCTCGACAAGCTCCACAGAGCTGCTGGTGGGTAAGT 338

Db 222 GTACCACGTCATGAGAGAGATCTCGACAAGCTCCACAGAGCTGCTGGTGGGTAAGT 281

QY 339 CCCGAGAAAGGATCTCATCGTCATGCTCAGGAGACCTGATGTGAACAAGAGGAGCAAGCA 398

Db 282 CCCGAGAAAGGATCTCATCGTCATGCTCAGGAGACCTGATGTGAACAAGAGGAGCAAGCA 341

QY 399 AAGAGGAGCTGCTTACATCTGGCTGCTGCCAATGGGAATTCAGAGTAGTAAACTGCT 458

Db 342 AAGAGGAGCTGCTTACATCTGGCTGCTGCCAATGGGAATTCAGAGTAGTAAACTGCT 401

QY 459 GCTGCAGACAGCATGCTCAACTTAATGTCTTGACAAACAAAGAGGAGCAGCTTCTGACAAA 518

Db 402 GCTGCAGACAGCATGCTCAACTTAATGTCTTGACAAACAAAGAGGAGCAGCTTCTGACAAA 461

QY 519 GGGCGTACAATGCCAGGAGATGAATGCGTAAATGTTGCTGGAAACATGCGACTGATCC 578

Db 462 GGGCGTACAATGCCAGGAGATGAATGCGTAAATGTTGCTGGAAACATGCGACTGATCC 521

QY 579 AATATTTCCAGATGATGGAATPACCACTCTACACTATGCTGTCTACATGAAGATAA 638

Db 522 AATATTTCCAGATGATGGAATPACCACTCTACACTATGCTGTCTACATGAAGATAA 581

QY 639 ATTATGGCCAAAAGCAGCTGCTTTATACGGTGTGATATCGAATCAAAAAACAGCATGG 698

Db 582 ATTATGGCCAAAAGCAGCTGCTTTATACGGTGTGATATCGAATCAAAAAACAGCATGG 641

QY 699 CCTCACACCATGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAAT 758

Db 642 CCTCACACCATGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAAT 701

QY 759 CAAGAAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATATTCG 818

Db 702 CAAGAAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATATTCG 761

QY 819 TGTATGTTGTGATCAGCAAGTATAGTCAGCCCTTACTTTCAGCAAGATGTTGATATTC 878

Db 762 TGTATGTTGTGATCAGCAAGTATAGTCAGCCCTTACTTTCAGCAAGATGTTGATATTC 821

QY 879 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933

Db 822 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 876

RESULT 10

ABL95290

ID ABL95290 standard; cDNA; 879 BP.

XX

XX Example 11; Page 475; 691pp; English.

PS The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention

SQ Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;

Query Match 78.6%; Score 733; DB 7; Length 879;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	99	CAGGGGAGCGGAGAGCAACGCTGGGCACTTCGGAGACCAACGACTCTCTGTGAA	158
DB	42	CAGGGGAGCGGAGAGCAACGCTGGGCACTTCGGAGACCAACGACTCTCTGTGAA	101
QY	159	GACGCTTGGGAGCAAGAGGTGAAGTGTGTGCTGCCACTGCTTCCCTGCTGCAGGGGGAG	218
DB	102	GACGCTTGGGAGCAAGAGGTGAAGTGTGTGCTGCCACTGCTTCCCTGCTGCAGGGGGAG	161
QY	219	CGGCAAGAGCAACGCTGGGCGCTTGGGAGACTACGATGACAGCGCTTCATGGATCCAG	278
DB	162	CGGCAAGAGCAACGCTGGGCGCTTGGGAGACTACGATGACAGCGCTTCATGGATCCAG	221
QY	279	GTACACGCTCCATGAGAGAGTCTGGACAAGCTCCACAGCTGCTGGTGGGTAAAGT	338
DB	222	GTACACGCTCCATGAGAGAGTCTGGACAAGCTCCACAGCTGCTGGTGGGTAAAGT	281
QY	339	CCCCAGAGAGATCTCATGCTCATGCTCAGGACACGATGTGAACAGGGGACAGCA	398
DB	282	CCCCAGAGAGATCTCATGCTCATGCTCAGGACACGATGTGAACAGGGGACAGCA	341
QY	399	AAAGAGGAGTCTCTACACTCTGGCTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCGT	458
DB	342	AAAGAGGAGTCTCTACACTCTGGCTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCGT	401
QY	459	GCTGACAGACGATGTCAACTTAATGTCTCTGACAAAGAGGACAGCTCTGACAAA	518
DB	402	GCTGACAGACGATGTCAACTTAATGTCTCTGACAAAGAGGACAGCTCTGACAAA	461
QY	519	GGCCGTACAAATGCCAGGAGAGTGAATGTGCTTGAATGTGCTGGAACATGCACTGATCC	578
DB	462	GGCCGTACAAATGCCAGGAGAGTGAATGTGCTTGAATGTGCTGGAACATGCACTGATCC	521
QY	579	AAATATTCAGATGATGGAATACCACTACACTATGCTGTCTACAAATGAAGTAA	638
DB	522	AAATATTCAGATGATGGAATACCACTACACTATGCTGTCTACAAATGAAGTAA	581
QY	639	ATTAATGCCAAGCACTGCTTATACGCTGCTGATATCGAATCAAAACAAAGCAGTGG	698
DB	582	ATTAATGCCAAGCACTGCTTATACGCTGCTGATATCGAATCAAAACAAAGCAGTGG	641
QY	699	CCTCACACCTGCTACTTGGTATACATGAGCAAAACAGCAAGTGGTGAATTTTAAAT	758
DB	642	CCTCACACCTGCTACTTGGTATACATGAGCAAAACAGCAAGTGGTGAATTTTAAAT	701
QY	759	CAAGAAAAGCGAATTAATGCGCTGGATAGATATGGAAGTCTCTCACTATGTC	818
DB	702	CAAGAAAAGCGAATTAATGCGCTGGATAGATATGGAAGTCTCTCACTATGTC	761
QY	819	TGTATGTTGTGATCAGCAAGTATAGTCAGGCTCTACTTGGCAAAATGTTGATGATC	878
DB	762	TGTATGTTGTGATCAGCAAGTATAGTCAGGCTCTACTTGGCAAAATGTTGATGATC	821
QY	879	TTCTCAAGATCTGGAAGCGCCAGAGATATGCTGTTCTAGTCATCATG 933	
DB	822	TTCTCAAGATCTGGAAGCGCCAGAGATATGCTGTTCTAGTCATCATG 876	

RESULT 13

ADAI1393
XX ADAI1393 standard; cDNA; 879 BP.
XX AC ADAI1393;
XX DT 06-NOV-2003 (first entry)
XX DE Human breast cancer specific full length cDNA B305D-A ORF.
XX ss; gene; human; breast cancer; cytostatic; tumour; gene therapy.
XX Homo sapiens.
XX US2002165371-A1.
XX 07-NOV-2002.
XX 07-AUG-2001; 2001US-00924400.
XX 11-JAN-1996; 96US-00585392.
XX 10-JAN-1997; 97WO-US000485.
XX 09-APR-1997; 97US-00838762.
XX 11-DEC-1997; 97US-00991789.
XX 17-APR-1998; 98US-00062451.
XX 09-APR-1999; 99US-00289198.
XX 28-OCT-1999; 99US-00423755.
XX 23-MAR-2000; 2000US-00534825.
XX 24-MAY-2000; 2000US-00577505.
XX 08-JUN-2000; 2000US-00590583.
XX 26-OCT-2000; 2000US-00699295.
XX 16-MAR-2001; 2001US-00810936.
XX (FRUD/) FRUDAKIS T N.
XX (REED/) REED S G.
XX (SMIT/) SMITH J M.
XX (MISH/) MISHNER L E.
XX (DILL/) DILLON D C.
XX (RETT/) RETTER M W.
XX (WANG/) WANG A.
XX (SKEI/) SKEIKY Y A W.
XX (HARL/) HARLOCKER S L.
XX (DAYC/) DAY C H.
XX (LISX/) LI S X.
XX (DENG/) DENG T.
XX Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
XX Wang A, Skeiky YAW, Harlocker SL, Day CH, Li SX, Deng T;
XX WPI; 2003-247262/24.
XX P-PSDB; ADAI1394.
XX New breast tumor proteins nucleic acids encoding such proteins, useful in
XX diagnosing, preventing and/or treating diseases such as cancer,
XX particularly breast cancer, and as markers for detecting the presence of
XX a cancer.
XX Claim 1; Page 149; 190pp; English.
XX The invention relates to a breast tumour polynucleotide selected from one
XX of the 275 fully defined nucleotide sequences (a) given in the
XX specification, including their complements, sequences consisting of at
XX least 20 contiguous residues of a sequence in (a), sequences that
XX hybridise to a sequence in (a) under moderately stringent conditions,
XX sequences having at least 75% or 90% identity to a sequence in (a), or
XX degenerate variants of a sequence in (a). Also included are an isolated
XX polypeptide (II) comprising an amino acid sequence selected from
XX sequences encoded by (a), sequences having at least 70% or 90% identity
XX to a sequence encoded by (a), sequences of 30 fully defined amino acid
XX sequences (c), and sequences having at least 70% or 90% identity to a
XX sequence in (c), expression vectors comprising (a), a host cell
XX transformed or transfected with the expression vector, an isolated
XX antibody or its antigen-binding fragment that specifically binds to (II),

a method for detecting the presence of a cancer in a patient, a fusion protein comprising at least one polypeptide (ii), an oligonucleotide that hybridises to (a), under moderately stringent conditions, a method for stimulating and/or expanding t cells specific for a tumour protein (by contacting t cells with at least one component selected from (a), (ii) and antigen-presenting t cells that express (ii)), an isolated t cell population comprising t cells prepared from as detailed above, a method for stimulating an immune response or treating cancer in a patient by administering a composition comprising (a), (ii), the vector, cells or the antibodies, and a method for inhibiting the development of a cancer in a patient. The polynucleotides may be used in the design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells. The breast tumour proteins are useful as markers to indicate the presence or absence of a cancer, such as breast cancer, and in the detection of other cancers. Compositions comprising the breast tumour proteins are useful in diagnosing, preventing and/or treating diseases such as cancer, particularly breast cancer. The present sequence is a breast cancer specific cDNA of the invention.

Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other; XX

Query Match 78.6%; Score 733; DB 7; Length 879;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels

Qy	99	CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCAACAACGATCTCTCTGTGAA	158
Db	42	CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCAACAACGATCTCTCTGTGAA	101
Qy	159	GAGCCTTGGGAGCAAGAGGTGCAAGTGTGTGCGCACTGCTTCCCTGCTGCAAGGGGGAG	218
Db	102	GACGCTTGGGAGCAAGAGGTGCAGTGTGTGCGCACTGCTTCCCTGCTGCAAGGGGGAG	161
Qy	219	CGGCAAGAGCAACGTGGGCGCTTGGGAGACTACGATCAGAGCGCCTTCATGATCCGAG	278
Db	162	CGGCAAGAGCAACGTGGTGCCTTGGGAGACTACGATCAGAGCGCCTTCATGATCCGAG	221
Qy	279	GTACACAGCTCCATGGAGAGACTCTGGACAAGCTCCAAGAGCTGCTGGTGGGGTAAAGT	338
Db	222	GTACCAAGCTCCATGGAGAGACTCTGGAACAAGCTCCAAGAGCTGCTGGTGGGGTAAAGT	281
Qy	339	CCCCAGAAAGGATCTCATCTGTCATGCTCAGGGACACTGATGTGAACAAGAGGACCAAGCA	398
Db	282	CCCCAGAAAGGATCTCATCTGTCATGCTCAGGGACACGGATGTGAACAAGAGGACCAAGCA	341
Qy	399	AAAGAGGACTGCTTACATCTGGCCCTCTGCCAATGGGAATTCAGAAAGTACTAAACTCGT	458
Db	342	AAAGAGGACTGCTTACATCTGGCCCTCTGCCAATGGGAATTCAGAAAGTACTAAACTCGT	401
Qy	459	GCTGGACAGACGATGTCAACTTAATGTCTTGAACAACAAAAGAGGACAGCTCTCGACAA	518
Db	402	GCTGGACAGACGATGTCAACTTAATGTCTTGAACAACAAAAGAGGACAGCTCTCGACAA	461
Qy	519	GGCGGTACAAATGCCAGGAAGATGAATGTGGTGTAAATGTTGCTGGAAACATGGCACTGATCC	578
Db	462	GGCGGTACAAATGCCAGGAAGATGAATGTGGTGTAAATGTTGCTGGAAACATGGCACTGATCC	521
Qy	579	AAATATTCCAGATGAGTATGGAAATACCACTCTACACTGTGCTPACAAATGAAGATAA	638
Db	522	AAATATTCCAGATGAGTATGGAAATACCACTCTACACTGTGCTPACAAATGAAGATAA	581
Qy	639	ATTAATGGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAAGCATGG	698
Db	582	ATTAATGGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAAGCATGG	641
Qy	699	CCTCACACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGTGAAAATTTTAAAT	758
Db	642	CCTCACACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGTGAAAATTTTAAAT	701
Qy	759	CAAGAAAAAGCGAAATTTAAATCGCGCTGGATAGATATGGAGAAACTGCTCTCATCTTGC	818
Db	702	CAAGAAAAAGCGAAATTTAAATCGCGCTGGATAGATATGGAGAAACTGCTCTCATACTTGC	761

Qy	819	TGTA	TGTTGTG	GATCAG	CAAGTAT	AGTCAG	CCCTCT	ACTTTG	AGCAAA	AACTT	CGATCT	ATC	878
Db	762	TGTAT	TGTTGTG	GATCAG	CAAGTAT	AGTCAG	CCCTCT	ACTTTG	AGCAAA	AACTT	CGATCT	ATC	821
Qy	879	TTCT	CAAGAT	CTTGG	AAAG	ACGCG	CCAGAG	ATGAT	CTCTTT	CTTCT	TAGTCAT	CAATCATG	933
Db	822	TTCT	CAAGAT	CTTGG	AAAG	ACGCG	CCAGAG	ATGAT	CTCTTT	CTTCT	TAGTCAT	CAATCATG	876

RESULT 14

ADC15366
ID ADC15366 standard; DNA; 879 BP.

XX ADC15366:

18-DEC-20

DI 10 DEC 2003 (11:06 AM)
XX
DE Human breast tumour protein

DE Human breast tumour protein DNA, SEQ ID NO: 1
XX
YW Cytostatic: Gene therapy: breast cancer: breast

KW d8.
KW Cytostatic; gene therapy; breast cancer; breast cancer without protein, human

OS Homo sapiens.

CD
XX
PN
WO2003013431-
HOME PAGE

20-FEB-2003.

XX
PF 05-AUG-2002:

03-AUG-2002} 2002MS 000215Z
XX
07-AUG-2001: 2001US-00924400: PR

PR	01-AUG-2002	2002US-00079137
PR	20-FEB-2002	2002US-00079137
PR	02-AUG-2002	2002US-00212679

02-RUG-2002, 200202-00720
XX
PA (CORI-) CORIXA CORP

FA (CORI-) CORIATH CORI
XX
PI Rander GB Hirst SK

yy
PI Kalos MD;
PI Fanger GR, Hirst SN, Dillon DC, Roy IN, Dougherty ND, LeVine SM

AA
DR
WPI; 2003
yy

PT New polynucleotide, treating or preventing

XX
 PT
 treating or preventing cancer
 Pivotal 2015
 Pivotal 2015

PS Example 1; SEQ ID NO 314; 308pp; English
XX
CC The present invention relates to computer

the present invention relates to compositions and methods for the treatment and diagnosis of cancer, particularly breast cancer. The method for detecting the presence of a cancer in a patient comprises: obtaining a biological sample from the patient; contacting the biological sample with a binding agent that binds to the polypeptide; detecting in the sample an amount of the polypeptide that binds to the binding agent; and comparing the amount of the polypeptide to a predetermined cut-off value. Treating breast cancer comprises administering a composition comprising breast tumour proteins and nucleic acids, which stimulates and/or expands T cells specific for the tumour protein. The present sequence was used to illustrate the invention.

Sequence: 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;

Query Match 78.6%; Score 733; DB 9; Length 879;

Best Local Similarity	99.8%	Pred. No. 0;
Matches 833: Conservative	0;	Mismatches
		2; Indels

99 CAGGGGAGGGGCAAGAGCAAGCTGGGCACTTCTGGAGACCAACGACTCTCTGTGAA 158

23 CAGGGGAGGGGCAAGAGCAACGTGGGCACCTTCTGAGAGCCAAACGATCCTCTGTGAA 101
 42 CAGGGGAGGGGCAAGAGCAACGTGGGCACCTTCTGAGAGCCAAACGATCCTCTGTGAA 101

159 GAGCTTGGAGGCA AGAGGTGCAAGTGTGTCTGCCCTGCTTCCCCTGCTGCAGGGGAG 218

[illegible][illegible]

```
QY 219 CGGCAAGAGCAACGCTGGCGCTTGGGAGACTACGATGACAGCGCTTTCATGATCCAG 278
|
|
|
Db 162 CGGCAAGAGCAACGCTGGCTTGGGAGACTACGATGACAGCGCTTTCATGATCCAG 221
|
|
|
QY 279 GTACCAAGTCCATGGAGAGACTCTGGAAGACTCCAGAGCTGCTGGTGGGTAAAGT 338
|
|
|
Db 222 GTACCAAGTCCATGGAGAGACTCTGGAAGACTCCAGAGCTGCTGGTGGGTAAAGT 281
|
|
|
QY 339 CCCAGAGAGGATCTCATCTGCTCAGGACATGATGTGAACAAGAGGAGCAAGCA 396
|
|
|
Db 282 CCCAGAGAGGATCTCATCTGCTCAGGACATGATGTGAACAAGAGGAGCAAGCA 341
|
|
|
QY 399 AAAGAGAGCTCTCATCTGCTGCTGCAATGGGAATTCAGAGTCTGTAAGTCTGT 458
|
|
|
Db 342 AAAGAGAGCTCTCATCTGCTGCTGCAATGGGAATTCAGAGTCTGTAAGTCTGT 401
|
|
|
QY 459 GCTGGACAGAGTGTCAACTTAATGCTTGTGACCAACAAAAGAGGACAGCTCTGACAAA 518
|
|
|
Db 402 GCTGGACAGAGTGTCAACTTAATGCTTGTGACCAACAAAAGAGGACAGCTCTGACAAA 461
|
|
|
QY 519 GGCGGTACATGCCAGGAGAGTGTGCGTTAATGCTTGTGACCAATGCCACTGATCC 578
|
|
|
Db 462 GGCGGTACATGCCAGGAGAGTGTGCGTTAATGCTTGTGACCAATGCCACTGATCC 521
|
|
|
QY 579 AAATATTCAGATGATGGAATACCACTCTACACTATGCTCTACAAATGAAGATAA 638
|
|
|
Db 522 AAATATTCAGATGATGGAATACCACTCTACACTATGCTCTACAAATGAAGATAA 581
|
|
|
QY 639 ATTAATGCCAAAAGCACTGCTTATACGCTGTGATATGGAATCAAAAACAGCATGG 698
|
|
|
Db 582 ATTAATGCCAAAAGCACTGCTTATACGCTGTGATATGGAATCAAAAACAGCATGG 641
|
|
|
QY 699 CCTCACACCTGCTTACTTGTATACATGACCAAAAACAGCAAGTGTGAAATTTTAAAT 758
|
|
|
Db 642 CCTCACACCTGCTTACTTGTATACATGACCAAAAACAGCAAGTGTGAAATTTTAAAT 701
|
|
|
QY 759 CAAGAAAAAGCAATTTAAATGCGCTGATATGGAAGAACTGCTCTCATCTGTC 818
|
|
|
Db 702 CAAGAAAAAGCAATTTAAATGCGCTGATATGGAAGAACTGCTCTCATCTGTC 761
|
|
|
QY 819 TGTATGTTGTGATCAGCAAGTATAGTCAGCCCTTACTTGCAGCAAAATGTGATGATC 878
|
|
|
Db 762 TGTATGTTGTGATCAGCAAGTATAGTCAGCCCTTACTTGCAGCAAAATGTGATGATC 821
|
|
|
QY 879 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933
|
|
|
Db 822 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 876
|
|
|
RESULT 15
ADBI3981
ID ADBI3981 standard; cDNA; 879 BP.
XX
AC ADBI3981;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human prostate specific cDNA B305 splice variant #11 ORF.
XX
KW Human; ss; prostate specific cDNA; cytostatic; immunostimulant;
KW gene therapy; cell therapy; vaccine; T-cell epitope;
KW class I major histocompatibility complex allele; MHC; prostate cancer;
KW tumour; antigen presenting cell.
XX
OS Homo sapiens.
XX
PN US2003185830-A1.
XX
PD 02-OCT-2003.
XX
PF 12-NOV-2002; 2002US-00294025.
XX
PT 25-FEB-1997; 97US-00806099.
```

```
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
PR 09-MAY-2002; 2002US-00144678.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Stolk JA, Kalos MD;
XX
XX WPI; 2003-756193/71.
XX
XX P-PSDB; ADBI3982.
```

New isolated polypeptide for use in a vaccine for stimulating an immune response, or for treating or diagnosis cancer, preferably prostate cancer.

Example 11; Page; 101pp; English.

The invention relates to an isolated polypeptide comprising no more than 11-542 amino acids of ADBI3563 comprising a sequence ADBI4487. The polypeptides comprise a fragment ADBI3563 of that contain naturally processed T-cell epitopes for 3 class I major histocompatibility complex (MHC) alleles. ADBI3563 is a polypeptide encoded by a human prostate specific cDNA, one of 618 disclosed as new. Also included are nucleic acids encoding the proteins and peptides, expression vectors, a host cell transformed with the vector, an isolated antibody (or antigen binding fragment) that specifically binds to the protein or peptide, detecting the presence of a cancer in a patient (comprising contacting a patient sample with a binding agent that binds to the peptides or a polypeptide appearing as ADBI3558, detecting the amount of polypeptide that binds to the agent and comparing the amount of polypeptide to a predetermined cut-off value to determine the presence of cancer), a fusion protein comprising the peptides or proteins, stimulating or expanding T cells specific for a tumour protein comprising contacting T cells with the peptides or the isolated T cell population, creating prostate cancer in a patient comprising administering a composition comprising the peptides, nucleic acids, antibodies or compounds, determining the presence of a cancer in a patient and treating prostate cancer in a patient comprising incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated from a patient with the peptides or antigen presenting cells that express (the peptides so that the T cells proliferate and administering the proliferated T cells to the patient. the peptides (or an oligonucleotide that hybridises to nucleic acid encoding them), is used to detect the presence of cancer in a patient. The peptides, nucleic acids encoding, or antigen-presenting cells expressing the nucleic acid, are used to stimulate or expand T cells specific for a tumour protein. The peptides, nucleic acids, antibodies, fusion proteins, T cell populations or antigen presenting cells are used to stimulate an immune response or treat prostate cancer in a patient. The present sequence is a known CDNA

CC showing sequence similarity to one of the disclosed human prostate
CC specific cDNAs. Note: Except where otherwise indicated, the sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030185830.

XX
SQ Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;

Query Match 78.6%; Score 733; DB 9; Length 879;
Best Local Similarity 99.8%; Fred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	99	CAGGGGAGGGGCAAGAGCAACGTGGGCACCTCTGGAGACCAACAGACTCTCTGTGAA	158
DB	42	CAGGGGAGGGGCAAGAGCAACGTGGGCACCTCTGGAGACCAACAGACTCTCTGTGAA	101
QY	159	GAGCCTTGGGAGCAAGAGTGCAAGTGTCTGCCACTGCTCCCTGCTGCAAGGGGAG	218
DB	102	GAGCCTTGGGAGCAAGAGTGCAAGTGTCTGCCACTGCTCCCTGCTGCAAGGGGAG	161
QY	219	CGGCAAGAGCAACGTGGGCGCTTGGGAGACTACGATGACAGCGCTTTCATGGATCCCAG	278
DB	162	CGGCAAGAGCAACGTGGTCTGCTTGGGAGACTACGATGACAGCGCTTTCATGGATCCCAG	221
QY	279	GTACCACTCCATGGAGAGATCTGGACAAGCTCCACAGAGCTGCTGCTGGGGTAAAGT	338
DB	222	GTACCACTCCATGGAGAGATCTGGACAAGCTCCACAGAGCTGCTGCTGGGGTAAAGT	281
QY	339	CCCAGAAAGATCTCATCTCTCAGGGACACTGTGTGAACAAGAGGACCAAGCA	398
DB	282	CCCAGAAAGATCTCATCTCTCAGGGACACTGTGTGAACAAGAGGACCAAGCA	341
QY	399	AAAGAGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCGT	458
DB	342	AAAGAGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCGT	401
QY	459	GCTGGACAGAGTCAACTTAATGCTTGCACAAAAGAGGACGCTCTGACAA	518
DB	402	GCTGGACAGAGTCAACTTAATGCTTGCACAAAAGAGGACGCTCTGACAA	461
QY	519	GGCGTACAAATCCAGGAAGATGAATGTGGTTAATGTTCTGGAAATGGCACTGATCC	578
DB	462	GGCGTACAAATCCAGGAAGATGAATGTGGTTAATGTTCTGGAAATGGCACTGATCC	521
QY	579	AAATATTCAGATGAGTGAATACCACTCTACACTATGCTGTCTACATGAAGATAA	638
DB	522	AAATATTCAGATGAGTGAATACCACTCTACACTATGCTGTCTACATGAAGATAA	581
QY	639	ATTAATGCCAAAGCACTGCTCTTATACGCTGTGATCGAATCAAAAACCAAGCATGG	698
DB	582	ATTAATGCCAAAGCACTGCTCTTATACGCTGTGATCGAATCAAAAACCAAGCATGG	641
QY	699	CCTCACACCACTGCTACTTGTGTATACATGAGCAAAAACAGCAAGTGTGAAATTTTAAAT	758
DB	642	CCTCACACCACTGCTACTTGTGTATACATGAGCAAAAACAGCAAGTGTGAAATTTTAAAT	701
QY	759	CAAGAAAAGGAAATTTAAATGCGTGTGATGATGGAAGACTGCTCTCATCTTGC	818
DB	702	CAAGAAAAGGAAATTTAAATGCGTGTGATGATGGAAGACTGCTCTCATCTTGC	761
QY	819	TGTATGTTGTGATCAGCAAGTATAGTCAGCCCTCTACTTTGAGCAAAATGTTGATGTATC	878
DB	762	TGTATGTTGTGATCAGCAAGTATAGTCAGCCCTCTACTTTGAGCAAAATGTTGATGTATC	821
QY	879	TTCTCAGATCTGGAAGACCGCCAGAGAGTATGCTGTTTCTAGTCATCATG	933
DB	822	TTCTCAGATCTGGAAGACCGCCAGAGAGTATGCTGTTTCTAGTCATCATG	876

Search completed: April 30, 2004, 14:21:14
Job time : 428 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 14:06:23 ; Search time 97 Seconds
(without alignments)
5337.827 Million cell updates/sec

Title: US-10-079-137B-343

Perfect score: 933

Sequence: 1 atcggtggtgaggttgattc.....tggtttctagtcattcatcg 933

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTCUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	733	78.6	879	4	US-09-439-313-531
2	733	78.6	879	4	US-09-636-215-531
3	733	78.6	879	4	US-09-685-166A-531
4	733	78.6	879	4	US-09-429-755-314
5	733	78.6	1852	4	US-09-439-313-530
6	733	78.6	1852	4	US-09-636-215-530
7	733	78.6	1852	4	US-09-685-166A-530
8	733	78.6	1852	4	US-09-429-755-313
9	646	69.2	1851	3	US-08-991-789A-291
10	646	69.2	1851	4	US-09-439-313-366
11	646	69.2	1851	4	US-09-062-451-291
12	646	69.2	1851	4	US-09-062-451-292
13	646	69.2	1851	4	US-09-352-616A-366
14	646	69.2	1851	4	US-09-289-198-291
15	646	69.2	1851	4	US-09-289-198-292
16	646	69.2	1851	4	US-09-636-215-366
17	646	69.2	1851	4	US-09-685-166A-366
18	646	69.2	1851	4	US-09-429-755-291
19	646	69.2	1851	4	US-09-429-755-292
20	646	69.2	2184	4	US-09-439-313-370
21	646	69.2	2184	4	US-09-062-451-296
22	646	69.2	2184	4	US-09-352-616A-370
23	646	69.2	2184	4	US-09-289-198-296
24	646	69.2	2184	4	US-09-636-215-370
25	646	69.2	2184	4	US-09-685-166A-370
26	646	69.2	2184	4	US-09-429-755-296
27	366	39.2	454	3	US-08-991-789A-211

C 28	366	39.2	454	4	US-09-062-451-211	Sequence 211, App
C 29	366	39.2	454	4	US-09-598-326-211	Sequence 211, App
C 30	366	39.2	454	4	US-09-289-198-211	Sequence 211, App
C 31	366	39.2	454	4	US-09-429-755-211	Sequence 211, App
C 32	304	32.6	1855	4	US-09-439-313-371	Sequence 371, App
C 33	304	32.6	1855	4	US-09-062-451-297	Sequence 297, App
C 34	304	32.6	1855	4	US-09-352-616A-371	Sequence 371, App
C 35	304	32.6	1855	4	US-09-289-198-297	Sequence 297, App
C 36	304	32.6	1855	4	US-09-636-215-371	Sequence 371, App
C 37	304	32.6	1855	4	US-09-685-166A-371	Sequence 371, App
C 38	304	32.6	1855	4	US-09-429-755-297	Sequence 297, App
C 39	201	21.5	495	4	US-09-833-381-1146	Sequence 1146, App
C 40	120	12.9	1059	4	US-09-439-313-372	Sequence 372, App
C 41	120	12.9	1059	4	US-09-352-616A-372	Sequence 372, App
C 42	120	12.9	1059	4	US-09-289-198-298	Sequence 298, App
C 43	120	12.9	1059	4	US-09-636-215-372	Sequence 372, App
C 44	120	12.9	1059	4	US-09-685-166A-372	Sequence 372, App
C 45	120	12.9	1059	4	US-09-429-755-298	Sequence 298, App

ALIGNMENTS

RESULT 1

US-09-439-313-531
; Sequence 531, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 531
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-531

Query Match 78.6%; Score 733; DB 4; Length 879;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	99	CAGGGGCGGCGGCAAGAGCAAGTGGCGACTTCTGGAGACCAACAGACTCTCTGTGAA	158
Db	42	CAGGGGCGGCGGCAAGAGCAAGTGGCGACTTCTGGAGACCAACAGACTCTCTGTGAA	101
Qy	159	GACGCTTGGGACCAAGAGTGCAGTGGTGGTCCACTGCTTCCCTGTCAGGGGGAG	218
Db	102	GACGCTTGGGACCAAGAGTGCAGTGGTGGTCCACTGCTTCCCTGTCAGGGGGAG	161
Qy	219	CGGACAGCAAGTGGGCGGCTTGGGAGCTACCATGACGCGCTTCATGGATCCAG	278
Db	162	CGGACAGCAAGTGGGCGGCTTGGGAGCTACCATGACGCGCTTCATGGATCCAG	221
Qy	279	GTACCAAGTCCATGGAGAGATCTGGACAAGTCCACAGAGCTGCTGGGGTAAAGT	338
Db	222	GTACCAAGTCCATGGAGAGATCTGGACAAGTCCACAGAGCTGCTGGGGTAAAGT	281
Qy	339	CCCCGAAAGGATCTCATGCTCACTGCTCAGGACACTGATGTGACACAGGGGCAAGCA	398

Db 282 CCCAGAAAGGATCTCATGTCATGTCAGGACACGATGTGAACAGAGGGACACGA 341
QY 399 AAGAGGACTGCTTACATCTGCGCTCTGCGCTTCCCAATGGAAATCAGAAAGTAGTAAACTCGT 458
Db 342 AAGAGGACTGCTTACATCTGCGCTCTGCGCTTCCCAATGGAAATCAGAAAGTAGTAAACTCGT 401
QY 459 GCTGGACACAGCATGTCACCTTAAATGCTCTGACACAAAGAGAGGACAGCTCTGACAAA 518
Db 402 GCTGGACACAGCATGTCACCTTAAATGCTCTGACACAAAGAGAGGACAGCTCTGACAAA 461
QY 519 GCGCGTACAAATGCCAGAAAGATGATGTCGTTAATGTTGCTGGAAACATGGCACTGATCC 578
Db 462 GCGCGTACAAATGCCAGAAAGATGATGTCGTTAATGTTGCTGGAAACATGGCACTGATCC 521
QY 579 AATATTTCCAGATGAGTATGGAATACCACTCTACACTATGCTCTCAATGAAGATAA 638
Db 522 AATATTTCCAGATGAGTATGGAATACCACTCTACACTATGCTCTCAATGAAGATAA 581
QY 639 ATTAATGGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 698
Db 582 ATTAATGGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 641
QY 699 CCTCACACCACTGCTACTTGGTATATACATGACGCAAAACAGCAAGTGGTGAATTTTAA 758
Db 642 CCTCACACCACTGCTACTTGGTATATACATGACGCAAAACAGCAAGTGGTGAATTTTAA 701
QY 759 CAAGAAAAAGCGAATTTAAATGCGTGGATAGATATGGAAGAACTGCTCTCATATTCG 818
Db 702 CAAGAAAAAGCGAATTTAAATGCGTGGATAGATATGGAAGAACTGCTCTCATATTCG 761
QY 819 TGTATGTTGGATACAGCAAGTATGATGAGCCCTCTACTTGAGCAAAATGTTGATGATC 878
Db 762 TGTATGTTGGATACAGCAAGTATGATGAGCCCTCTACTTGAGCAAAATGTTGATGATC 821
QY 879 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG 933
Db 822 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG 876

RESULT 2

US-09-636-215-531

; Sequence 531, Application US/09636215

; Patent No. 6620922

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John H.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 21021-42717C17

; CURRENT APPLICATION NUMBER: US/09/636,215

; CURRENT FILING DATE: 2000-08-10

; NUMBER OF SEQ ID NOS: 852

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 531

; LENGTH: 879

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-636-215-531

Query Match 78.8%; Score 733; DB 4; Length 879;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGCAAGAGCAACCTGGGCACTTCTGGAGACCAACAAGACTCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGAGCAACCTGGGCACTTCTGGAGACCAACAAGACTCTCTGTGAA 101
QY 159 GACGCTTGGAGACCAAGGTGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 218
Db 102 GACGCTTGGAGACCAAGGTGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 161
QY 219 CGGCAAGAGCAACCTGGGCGCTTGGGAGACTAGTACAGAGCGCTTCTATGATCCAG 278
Db 162 CGGCAAGAGCAACCTGGGCGCTTGGGAGACTAGTACAGAGCGCTTCTATGATCCAG 221
QY 279 GTACCAAGTCCATGGAGAAAGTCTGGCAAGCTCCAGAGCTGCTGTGGGGTAAAGT 338
Db 222 GTACCAAGTCCATGGAGAAAGTCTGGCAAGCTCCAGAGCTGCTGTGGGGTAAAGT 281
QY 339 CCCAGAAAGGATCTCATCTGTCATGCTCAGGACACTGTGTGAAACAAGAGGACAGCA 398
Db 282 CCCAGAAAGGATCTCATCTGTCATGCTCAGGACACTGTGTGAAACAAGAGGACAGCA 341
QY 399 AAGAGCACTGCTTACATCTGCGCTCTGCCAATGGGAATTCAGAACTAGTAAACTCGT 458
Db 342 AAGAGCACTGCTTACATCTGCGCTCTGCCAATGGGAATTCAGAACTAGTAAACTCGT 401
QY 459 GCTGGACACAGCATGTCACCTTAAATGCTTGGCAACAACAAGAGGACAGCTCTGACAA 518
Db 402 GCTGGACACAGCATGTCACCTTAAATGCTTGGCAACAACAAGAGGACAGCTCTGACAA 461
QY 519 GCGCGTACAATGCCAGAAAGTGAATGCGTTAATGTTGCTGGAACATGGCACTGATCC 578
Db 462 GCGCGTACAATGCCAGAAAGTGAATGCGTTAATGTTGCTGGAACATGGCACTGATCC 521
QY 579 AATATTTCCAGATGAGTATGGAATACCACTCTACACTATGCTCTACAAATGAGATAA 638
Db 522 AATATTTCCAGATGAGTATGGAATACCACTCTACACTATGCTCTACAAATGAGATAA 581
QY 639 ATTAATGGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 698
Db 582 ATTAATGGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 641
QY 699 CCTCACACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTAA 758
Db 642 CCTCACACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTAA 701
QY 759 CAAGAAAAAGCGAATTTAAATGCGTGGATAGATATGGAAGAACTGCTCTCATATTCG 818
Db 702 CAAGAAAAAGCGAATTTAAATGCGTGGATAGATATGGAAGAACTGCTCTCATATTCG 761
QY 819 TGTATGTTGGATACAGCAAGTATGATGAGCCCTCTACTTGAGCAAAATGTTGATGATC 878
Db 762 TGTATGTTGGATACAGCAAGTATGATGAGCCCTCTACTTGAGCAAAATGTTGATGATC 821
QY 879 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG 933
Db 822 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG 876

RESULT 3

US-09-685-166A-531

; Sequence 531, Application US/09685166A

; Patent No. 6630305

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi


```

; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Renger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 531
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-531

Query Match 78.6%; Score 733; DB 4; Length 879;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 99 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCAACGACTCCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCAACGACTCCTCTGTGAA 101

Qy 159 GACGCTTGGAGCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 218
Db 102 GACGCTTGGAGCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 161

Qy 219 CGGCAAGAGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 398
Db 282 CGGCAAGAGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 341

Qy 399 AAGGAGGACTGCTACATCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCT 458
Db 342 AAGGAGGACTGCTACATCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCT 401

Qy 459 GCTGGACAGAGTGTCAACTTAAATGTCTTGAACAACAAAGAGGACAGCTCTGACAAA 518
Db 402 GCTGGACAGAGTGTCAACTTAAATGTCTTGAACAACAAAGAGGACAGCTCTGACAAA 461

Qy 519 GCGCGTACAAATGCCAGGAGAGTGAATGTGCGTTAATGTGCTGGAACATGGCAGTATCC 578
Db 462 GCGCGTACAAATGCCAGGAGAGTGAATGTGCGTTAATGTGCTGGAACATGGCAGTATCC 521

; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Renger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 531
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-531

Query Match 78.6%; Score 733; DB 4; Length 879;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 99 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCAACGACTCCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCAACGACTCCTCTGTGAA 101

Qy 159 GACGCTTGGAGCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 218
Db 102 GACGCTTGGAGCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 161

Qy 219 CGGCAAGAGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 398
Db 282 CGGCAAGAGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 341

Qy 399 AAGGAGGACTGCTACATCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCT 458
Db 342 AAGGAGGACTGCTACATCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCT 401

Qy 459 GCTGGACAGAGTGTCAACTTAAATGTCTTGAACAACAAAGAGGACAGCTCTGACAAA 518
Db 402 GCTGGACAGAGTGTCAACTTAAATGTCTTGAACAACAAAGAGGACAGCTCTGACAAA 461

Qy 519 GCGCGTACAAATGCCAGGAGAGTGAATGTGCGTTAATGTGCTGGAACATGGCAGTATCC 578
Db 462 GCGCGTACAAATGCCAGGAGAGTGAATGTGCGTTAATGTGCTGGAACATGGCAGTATCC 521

; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Renger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 531
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-531

Query Match 78.6%; Score 733; DB 4; Length 879;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 99 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCAACGACTCCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCAACGACTCCTCTGTGAA 101

Qy 159 GACGCTTGGAGCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 218
Db 102 GACGCTTGGAGCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 161

Qy 219 CGGCAAGAGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 398
Db 282 CGGCAAGAGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 341

Qy 399 AAGGAGGACTGCTACATCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCT 458
Db 342 AAGGAGGACTGCTACATCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCT 401

Qy 459 GCTGGACAGAGTGTCAACTTAAATGTCTTGAACAACAAAGAGGACAGCTCTGACAAA 518
Db 402 GCTGGACAGAGTGTCAACTTAAATGTCTTGAACAACAAAGAGGACAGCTCTGACAAA 461

Qy 519 GCGCGTACAAATGCCAGGAGAGTGAATGTGCGTTAATGTGCTGGAACATGGCAGTATCC 578
Db 462 GCGCGTACAAATGCCAGGAGAGTGAATGTGCGTTAATGTGCTGGAACATGGCAGTATCC 521
```

```
QY 579 AAATATCCAGATGATGGAATACCACTCTACATATGCTGTCTACAAATGAAGATAA 638
Db 522 AAATATCCAGATGATGGAATACCACTCTACATATGCTGTCTACAAATGAAGATAA 581
QY 639 ATTAATGCCCAAGCACTGCTTTATACGCTGCTGATATGAATCAAAAAACAAGCATGG 698
Db 582 ATTAATGCCCAAGCACTGCTTTATACGCTGCTGATATGAATCAAAAAACAAGCATGG 641
QY 699 CCTCACACCACTGCTATCTGTATATACATGAGCAAAAAACAGCAAGTGTGAAATTTTAAAT 758
Db 642 CCTCACACCACTGCTATCTGTATATACATGAGCAAAAAACAGCAAGTGTGAAATTTTAAAT 701
QY 759 CAAGAAAAAGCGAATTTAAATGCGCTGATATGGAAGAACTCTCTCATATCTGC 818
Db 702 CAAGAAAAAGCGAATTTAAATGCGCTGATATGGAAGAACTCTCTCATATCTGC 761
QY 819 TGTATGTTGCGATCAGCAAGTATAGTACGCCCTCTACTTTGAGCAAAATGTTGATGTATC 878
Db 762 TGTATGTTGCGATCAGCAAGTATAGTACGCCCTCTACTTTGAGCAAAATGTTGATGTATC 821
QY 879 TTCTCAAGATCTGGAAGAGCGGCAGAGAGTATGCTGTTTCTAGTCATCATG 933
Db 822 TTCTCAAGATCTGGAAGAGCGGCAGAGAGTATGCTGTTTCTAGTCATCATG 876

RESULT 5
US-09-439-313-530
; Sequence 530, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Jennifer L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Salk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 530
; TYPE: DNA
; LENGTH: 1852
; ORGANISM: Homo sapiens
US-09-439-313-530

Query Match 78.6%; Score 733; DB 4; Length 1852;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGCAAGAGCACTGGGCACTTTGGAGACCAACAGCACTCTCTGTGAA 158
Db 771 CAGGGGAGCGGCAAGAGCACTGGGCACTTTGGAGACCAACAGCACTCTCTGTGAA 830
QY 159 GACCTTTGGAGCAAGAGGTCAGTGGTCCCTGCTCCCTGCTGCGAGGGGAG 218
Db 831 GACCTTTGGAGCAAGAGGTCAGTGGTCCCTGCTCCCTGCTGCGAGGGGAG 890
QY 219 CGGCAAGCAACTGGCGCTTTGGGAGACTACGATGACAGGCGCTTCATGATCCCGAG 278
Db 891 CGGCAAGCAACTGGCGCTTTGGGAGACTACGATGACAGGCGCTTCATGATCCCGAG 950
QY 279 GTACCACTCCATGGAGAGATCTGGACAGCTCCACAGAGCTGCTGCTGAGTAAAGT 338
Db 951 GTACCACTCCATGGAGAGATCTGGACAGCTCCACAGAGCTGCTGCTGAGTAAAGT 1010
```

```
QY 339 CCCGAGAAAGGATCTCATCTGTCATGCTCAGGACACTGATGTGAACAAGAGGCAAGCA 398
Db 1011 CCCGAGAAAGGATCTCATCTGTCATGCTCAGGACACTGATGTGAACAAGAGGCAAGCA 1070
QY 399 AAAGAGGACTCTCTACATCTGCTCTGCTCCATGCGGAATTCAGAACTAGTAAAACTGGT 458
Db 1071 AAAGAGGACTCTCTACATCTGCTCTGCTCCATGCGGAATTCAGAACTAGTAAAACTGGT 1130
QY 459 GCTGGACAGACCATGCTCAACTTAATGTCTTGACAAACAAAAAGAGGACAGCTCTGACAAA 518
Db 1131 GCTGGACAGACCATGCTCAACTTAATGTCTTGACAAACAAAAAGAGGACAGCTCTGACAAA 1190
QY 519 GCGCTGACATGCCAGGAAGATGAATGCGTTAATGTTGCTGGAAACATGGCAGCTGATCC 578
Db 1191 GCGCTGACATGCCAGGAAGATGAATGCGTTAATGTTGCTGGAAACATGGCAGCTGATCC 1250
QY 579 AAATATCCAGATGATGGAATACCACTCTACATATGCTGTCTACAATGAAGATAA 638
Db 1251 AAATATCCAGATGATGGAATACCACTCTACATATGCTGTCTACAATGAAGATAA 1310
QY 639 ATTAATGCCCAAGCACTGCTCTTATACGCTGCTGATATCGAATCAAAAAACAAGCATGG 698
Db 1311 ATTAATGCCCAAGCACTGCTCTTATACGCTGCTGATATCGAATCAAAAAACAAGCATGG 1370
QY 699 CCTCACACCACTGCTACTTTGATATACATGAGCAAAAAACAAGGTCGTGAAATTTTAAAT 758
Db 1371 CCTCACACCACTGCTACTTTGATATACATGAGCAAAAAACAAGGTCGTGAAATTTTAAAT 1430
QY 759 CAAGAAAAAGCGAATTTAAATGCGCTGATATGGAAGAACTCTCTCATATCTGC 818
Db 1431 CAAGAAAAAGCGAATTTAAATGCGCTGATATGGAAGAACTCTCTCATATCTGC 1490
QY 819 TGTATGTTGCGATCAGCAAGTATAGTACGCCCTCTACTTTGAGCAAAATGTTGATGTATC 878
Db 1491 TGTATGTTGCGATCAGCAAGTATAGTACGCCCTCTACTTTGAGCAAAATGTTGATGTATC 1550
QY 879 TTCTCAAGATCTGGAAGAGCGGCAGAGAGTATGCTGTTTCTAGTCATCATG 933
Db 1551 TTCTCAAGATCTGGAAGAGCGGCAGAGAGTATGCTGTTTCTAGTCATCATG 1605

RESULT 6
US-09-636-215-530
; Sequence 530, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 530
; LENGTH: 1852
```

Query Match	78.6%;	Score 733;	DB 4;	Length 1852;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 833;	Conservative	0;	Mismatches 2;	Indels 0;
Gaps 0;				
Qy	99	CAGGGGAGGGGCAAGAGCAACGTGGGCACCTTCTGGAGACACAAACGACTCCTCTGTGAA	158	
Db	771	CAGGGGAGGGGCAAGAGCAACGTGGGCACCTTCTGGAGACACAAACGACTCCTCTGTGAA	830	
Qy	159	GAGCCTTTGGGACCAAGAGGTCGAAGTGGTGTGCTGACACTGCTTCCCTGCTTGCAGGGGGAG	218	
Db	831	GACGCTTTGGGACCAAGAGGTCGAAGTGGTGTGCTGACACTGCTTCCCTGCTTGCAGGGGGAG	890	
Qy	219	CGGCAAGACCAACGTGGGCGCTTGGGAGACTACGATGACAGCGCCTTCATGATCCACG	278	
Db	891	CGGCAAGACCAACGTGGTGCCTTGGGAGACTACGATGACAGCGCCTTCATGATCCACG	950	
Qy	279	GTACCACGTCCATGGAGCAAGATCTGGACAAGCTCCACAGAGCTGCCCTGGTGGGGTAAAGT	338	
Db	951	GTACCACGTCCATGGAGCAAGATCTGGACAAGCTCCACAGAGCTGCCCTGGTGGGGTAAAGT	1010	
Qy	339	CCCAGAAAAGATCTCATGCTCATGCTTCAGGACACTGATGTGAACAAGAGGGACCAAGCA	398	
Db	1011	CCCAGAAAAGATCTCATGCTCATGCTTCAGGACACCGATGTGAACAAGAGGGACCAAGCA	1070	
Qy	399	AAAGAGCACTGCTCTACATCTGGGCTCTGCCAATGGGAATTCAGAACTAGTAAACTCGT	458	
Db	1071	AAAGAGCACTGCTCTACATCTGGGCTCTGCCAATGGGAATTCAGAACTAGTAAACTCGT	1130	
Qy	459	GCTGGACAGACGATGTCAACTTAATGTCCTTGACAACAAAAAGAGGACAGCTCTGACAAA	518	
Db	1131	GCTGGACAGACGATGTCAACTTAATGTCCTTGACAACAAAAAGAGGACAGCTCTGACAAA	1190	
Qy	519	GGCGGTACAATGCCAGGAAGATGAATGTCGTTAATGTTGCTGGACATGGCACTGATCC	578	
Db	1191	GGCGGTACAATGCCAGGAAGATGAATGTCGTTAATGTTGCTGGACATGGCACTGATCC	1250	
Qy	579	AAATATTCCAGATGAGTATGGAATACCACTACACTATGCTGTCTPACAATGAAGATAA	638	
Db	1251	AAATATTCCAGATGAGTATGGAATACCACTACACTATGCTGTCTPACAATGAAGATAA	1310	
Qy	639	ATTAAATGGCCCAAGCACTGCTCTTATACGCTGCTGATATCGATCAAAAAACAGCATGG	698	
Db	1311	ATTAAATGGCCCAAGCACTGCTCTTATACGCTGCTGATATCGATCAAAAAACAGCATGG	1370	
Qy	699	CCTCACACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTAAAT	758	
Db	1371	CCTCACACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTAAAT	1430	
Qy	759	CAAGAAAAAGCGAATTTAAATGGCTGGATAGATATGGAAGAACTGTCTCTCATCTTGC	818	
Db	1431	CAAGAAAAAGCGAATTTAAATGGCTGGATAGATATGGAAGAACTGTCTCTCATCTTGC	1490	
Qy	819	TGTATGTTGTGGATCAGCAAGTATAGTCGCCCTCTACTTTGAGCAAAATGTTGATGTATC	878	
Db	1491	TGTATGTTGTGGATCAGCAAGTATAGTCGCCCTCTACTTTGAGCAAAATGTTGATGTATC	1550	
Qy	879	TTCTCAAGATCTGGAAAGACGGCCAGAGATAGTGTGTTTCTTAGTCATCATCATG	933	
Db	1551	TTCTCAAGATCTGGAAAGACGGCCAGAGATAGTGTGTTTCTTAGTCATCATCATG	1605	

RESULT 7
US-09-685-166A-530
; Sequence 530, Application US/09685166A
; Patent No. 5630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.

Db	1251	AAATAATCCAGATGAGTATGGAAATACCACTTACACTATGCTGTCTACAATGAAGATAA	1310
QY	639	ATTAAATGGCCAAAGCACTGCTCTTATACGGTGTGTATCGAATCAAAAACAAGCATGG	698
Db	1311	ATTAAATGGCCAAAGCACTGCTCTTATACGGTGTGTATCGAATCAAAAACAAGCATGG	1370
QY	699	CCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAAT	758

237	QY	CGCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCAGGTACACACGTCATCGGA	296
944	Db	CGCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCAGGTACACGTCATCGGA	885
297	QY	AGATCTGGACAAGCTCCACAGAGCTGCTGTGGGTAAAGTCCCAAGAAAGGATCTCAT	356
884	Db	AGATCTGGACAAGCTCCACAGAGCTGCTGTGGGTAAAGTCCCAAGAAAGGATCTCAT	825
357	QY	CGTCTATGCTCAGGGACACTGATGTGAACAAGAGGGACAACGAAGAGGAGCTGCTCTACA	416
824	Db	CGTCTATGCTCAGGGACACTGATGTGAACAAGAGGGACAACGAAGAGGAGCTGCTCTACA	765
417	QY	TCGTGGCTCTGCAATGGGAATTCAGAAGTAGTAAAACTCGTCTGGACAGACGATGTCA	476
764	Db	TCGTGGCTCTGCAATGGGAATTCAGAAGTAGTAAAACTCGTCTGGACAGACGATGTCA	705
477	QY	ACTTAAATGTCCTTGACACAACAAAAGAGACAGCTCTGCACAAAGGCCGTACATGCCAGGA	536
704	Db	ACTTAAATGTCCTTGACACAACAAAAGAGACAGCTCTGCACAAAGGCCGTACATGCCAGGA	645
537	QY	AGATGAATGTGGTTAAATGTTCTGGAACTGGCACTGATCCAAATATTTCCAGATGAGTA	596
644	Db	AGATGAATGTGGTTAAATGTTCTGGAACTGGCACTGATCCAAATATTTCCAGATGAGTA	585
597	QY	TGGAATACCACTCTACACTACTGCTGTCTCAATGAAGATAAATTAATGGCCAAAGCACT	656
584	Db	TGGAATACCACTCTACACTACTGCTGTCTCAATGAAGATAAATTAATGGCCAAAGCACT	525
657	QY	GCTCTTATACGGTGTGATATCGAATCAAAAACAAGCATGGCCTCACACCACTGCTACT	716
524	Db	GCTCTTATACGGTGTGATATCGAATCAAAAACAAGCATGGCCTCACACCACTGCTACT	465
717	QY	TGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTTTAATCAAGAAAAGCGAATTT	776
464	Db	TGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTTTAATCAAGAAAAGCGAATTT	405
777	QY	AAATCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGTGTATGTTGGATCAGC	836
404	Db	AAATCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGTGTATGTTGGATCAGC	345
837	QY	AAATATAGTCAGCCCTCTACTTGAGCAAAATGTTGATATCTTCTCAGATCTGGAAAG	896
344	Db	AAATATAGTCAGCCCTCTACTTGAGCAAAATGTTGATATCTTCTCAGATCTGGAAAG	285
897	QY	ACGGCCAGAGAGTAGTGGTTCTTAGTCATCATCATG	933
284	Db	ACGGCCAGAGAGTAGTGGTTCTTAGTCATCATCATG	248

RESULT 10

US-09-439-313-366/c
; Sequence 366, Application US/09439313
; Patent No. 6329505

; FACILE NO. 0329303
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: DILLON, DAVIN C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan Louise

APPLICANT: Jiang Yuqi

APPLICANT: Reed, Steven G.

APPLICANT: Kalos, Michael

APPLICANT: Fanger, Gary

APPLICANT: Retter, Mark

APPLICANT: Solk, John

APPLICANT: Day, Craig

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

10 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C9

; CURRENT APPLICATION NUMBER: US/0:

;
; CURRENT FILING DATE: 1999

; NUMBER OF SEQ ID NOS: 575

```

; SEQ ID NO 366
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-366

```

Query Match 69.2%; Score 646; DB 4; Length 1851;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels

237	QY	CGCTGGGGAGACTACGATGACAGGGCTTCATGGATCCCGAGTACCACTGCTCCATGGAGA	236
944	Db	CGCTGGGGAGACTACGATGACAGGGCTTCATGGATCCCGAGTACCACTGCTCCATGGAGA	885
297	QY	AGATCTGGACAAGCTCCACAGAGCTGCCGTGGTGGGTAAAGTCCCCAGAAAGAGATCTCAT	356
884	Db	AGATCTGGACAAGCTCCACAGAGCTGCCGTGGTGGGTAAAGTCCCCAGAAAGAGATCTCAT	825
357	QY	CGTCACTGCTCAGGGACACTGATGTGGAACAAGAGGGACAAGCAAAAGAGGACTGCTCTTACA	416
824	Db	CGTCACTGCTCAGGGACACGGATGTGGAACAAGAGGGACAAGCAAAAGAGGACTGCTCTTACA	765
417	QY	TCCTGGCTCTCGCAATGGGAATCAGAAGTAGTAAAACTCGTGTGGACAGACGATGTCA	476
764	Db	TCCTGGCTCTCGCAATGGGAATCAGAAGTAGTAAAACTCGTGTGGACAGACGATGTCA	705
477	QY	ACTTAATGTCTTGACAAACAAAAGAGGACAGCTCTGACAAAGGCCGTACAAATGCCAGGA	536
704	Db	ACTTAATGTCTTGACAAACAAAAGAGGACAGCTCTGACAAAGGCCGTACAAATGCCAGGA	645
537	QY	AGATGAATGTGGTTATGTTGCTGGACATGGCACTGATCCAAATATTCACAGATGAGTA	596
644	Db	AGATGAATGTGGTTATGTTGCTGGACATGGCACTGATCCAAATATTCACAGATGAGTA	585
597	QY	TGGAAATACCACTCTTACACTATGCTGTCTCAATGAAGATAAAATTAATGGCCCAAAGCACT	656
584	Db	TGGAAATACCACTCTTACACTATGCTGTCTCAATGAAGATAAAATTAATGGCCCAAAGCACT	525
657	QY	GCTCTTATACGGTGTGATTCGAATCAAAAACAGACATGGCGCTCACACCACTGCTACT	716
524	Db	GCTCTTATACGGTGTGATTCGAATCAAAAACAGACATGGCGCTCACACCACTGCTACT	465
717	QY	TGGTATACATGACGAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAACGCAATTT	776
464	Db	TGGTATACATGACGAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAACGCAATTT	405
777	QY	AAATCGCGTGGATAGATATGGAAGAACTGCTCTCATCTTCTGTATGTTGGATCAGC	836
404	Db	AAATCGCGTGGATAGATATGGAAGAACTGCTCTCATCTTCTGTATGTTGGATCAGC	345
837	QY	AAATATAGTCAGCCCTCTACTTTGAGCAAAATGTTGATGATCTTCTCAAGATCTGGAAAG	896
344	Db	AAATATAGTCAGCCCTCTACTTTGAGCAAAATGTTGATGATCTTCTCAAGATCTGGAAAG	285
897	QY	ACGCCGACAGAGTATGCTGTTCTTAGTCATCATCATG	933
284	Db	ACGCCGACAGAGTATGCTGTTCTTAGTCATCATCATG	248

RESULT 11

US-09-062-451-291/c

; Sequence 291, Application US/09062451

; Patent No. 6344550

GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.

APPLICANT: Smith, John M.

APPLICANT: Reed, Steven G

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

CONCLUSIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER

NUMBER OF SEQUENCES: 297

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 291:
SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-062-451-291

Query Match 69.2%; Score 646; DB 4; Length 1851;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 237 CGCTTGGGAGACTACGATGACAGCGCTTCATGGATCCAGGTACACGTCATCGAGA 296
DB 944 CGCTTGGGAGACTACGATGACAGCGCTTCATGGATCCAGGTACACGTCATCGAGA 885
QY 297 AGATCTGGACAGCTCCACAGAGCTGCCTGGTGGGTAAGTCCCGAAGAGATCTCAT 356
DB 884 AGATCTGGACAGCTCCACAGAGCTGCCTGGTGGGTAAGTCCCGAAGAGATCTCAT 825
QY 357 CGTCATGCTCAGGACACTGATGTGAACAGAGGGACAGCAAGAGGAGCTGCTTACA 416
DB 824 CGTCATGCTCAGGACACTGATGTGAACAGAGGGACAGCAAGAGGAGCTGCTTACA 765
QY 417 TCTGGCCTCTGCCAATCGGAATTCAGAAAGTAGTAAACTCGTGTGACAGAGCATGTCA 476
DB 764 TCTGGCCTCTGCCAATCGGAATTCAGAAAGTAGTAAACTCGTGTGACAGAGCATGTCA 705
QY 477 ACTTAATGCTCTTGACAAACAAAGAGGACAGCTCTGACAAAGGCGGTACATGCCAGA 536
DB 704 ACTTAATGCTCTTGACAAACAAAGAGGACAGCTCTGACAAAGGCGGTACATGCCAGA 645
QY 537 AGATGAATGTCGTTAATGTTGCTGGAACATGCGCACTGATCCAAATATTCAGATGAGTA 596
DB 644 AGATGAATGTCGTTAATGTTGCTGGAACATGCGCACTGATCCAAATATTCAGATGAGTA 585
QY 597 TGGAAATACCACTACACTGCTCTACATGAAGTAATTAATGCGCAAGCACT 656
DB 584 TGGAAATACCACTACACTGCTCTACATGAAGTAATTAATGCGCAAGCACT 525
QY 657 GCTCTTATACGGTGTGATATCGAATCAAAACAAAGAGGAGCTGCTCAGCACTGCTACT 716
DB 524 GCTCTTATACGGTGTGATATCGAATCAAAACAAAGAGGAGCTGCTCAGCACTGCTACT 465
QY 717 TGGTATACATGACAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAACGGAATTT 776
DB 464 TGGTATACATGACAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAACGGAATTT 405
QY 777 AAATGGCTGGATAGATATGGAAGAGTGTCTCTCATCTTGTGTATGTTGGATCAGC 836
DB 404 AAATGGCTGGATAGATATGGAAGAGTGTCTCTCATCTTGTGTATGTTGGATCAGC 345
QY 837 AAGTATAGTCAGCCCTCTACTTGGACAAAATGTTGATGTATCTTCTCAAGATCTGGAAG 896

DB 344 AAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTATCTTCTCAAGATCTGGAAG 285
QY 897 ACGGCCACAGAGTATGCTGTTTCTAGTTCATCATCATG 933
DB 284 ACGGCCACAGAGTATGCTGTTTCTAGTTCATCATCATG 246

RESULT 12
US-09-062-451-292/c
Sequence 292, Application US/09062451
Patent No. 6344550
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 292:
SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-062-451-292

Query Match 69.2%; Score 646; DB 4; Length 1851;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 237 CGCTTGGGAGACTACGATGACAGCGCTTCATGGATCCAGGTACACGTCATCGAGA 296
DB 944 CGCTTGGGAGACTACGATGACAGCGCTTCATGGATCCAGGTACACGTCATCGAGA 885
QY 297 AGATCTGGACAGCTCCACAGAGCTGCCTGGTGGGTAAGTCCCGAAGAGATCTCAT 356
DB 884 AGATCTGGACAGCTCCACAGAGCTGCCTGGTGGGTAAGTCCCGAAGAGATCTCAT 825
QY 357 CGTCATGCTCAGGACACTGATGTGAACAGAGGGACAGCAAGAGGAGCTGCTTACA 416
DB 824 CGTCATGCTCAGGACACTGATGTGAACAGAGGGACAGCAAGAGGAGCTGCTTACA 765
QY 417 TCTGGCCTCTGCCAATCGGAATTCAGAAAGTAGTAAACTCGTGTGACAGAGCATGTCA 476
DB 764 TCTGGCCTCTGCCAATCGGAATTCAGAAAGTAGTAAACTCGTGTGACAGAGCATGTCA 705
QY 477 ACTTAATGCTCTTGACAAACAAAGAGGACAGCTCTGACAAAGGCGGTACATGCCAGA 536
DB 704 ACTTAATGCTCTTGACAAACAAAGAGGACAGCTCTGACAAAGGCGGTACATGCCAGA 645

QY 537 AGATGAATGTCGTTAAATGTTGCTGGAACTGGCACTGATCCAAATATTCAGATGAGTA 596
Db 644 AGATGAATGTCGTTAAATGTTGCTGGAACTGGCACTGATCCAAATATTCAGATGAGTA 595
QY 597 TGGAAATACCACTCTACACTATGCTGCTCAATGAAGATAAATTAATGCGCAAGCACT 656
Db 584 TGGAAATACCACTCTACACTATGCTGCTCAATGAAGATAAATTAATGCGCAAGCACT 525
QY 657 GCTCTTATACCGTGTGATATCGAATCAAAAAACAAGCATGGCCCTCACACCACTGCTACT 716
Db 524 GCTCTTATACCGTGTGATATCGAATCAAAAAACAAGCATGGCCCTCACACCACTGCTACT 465
QY 717 TGGTATACATGAGCAAAACAAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCGAATTT 776
Db 464 TGGTATACATGAGCAAAACAAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCGAATTT 405
QY 777 AAATGCGGTGATAGATGGAAGCACTGCTCTCATCTGCTGATGTTGTTGATGATCAGC 836
Db 404 AAATGCGGTGATAGATGGAAGCACTGCTCTCATCTGCTGATGTTGTTGATGATCAGC 345
QY 837 AAGTATAGTACGCTCTACTTGAGCAAAATGTTGATGATCTTCTCAAGATCTGGAAG 896
Db 344 AAGTATAGTACGCTCTACTTGAGCAAAATGTTGATGATCTTCTCAAGATCTGGAAG 285
QY 897 ACGGCCAGAGATGCTGTTTCTAGTCATCATG 933
Db 284 ACGGCCAGAGATGCTGTTTCTAGTCATCATG 248

RESULT 13

US-09-352-616A-366/c

; Sequence 366, Application US/09352616A

; Patent No. 6395278

; GENERAL INFORMATION:

; APPLICANT: Dillon, Davin C.

; APPLICANT: Harlocker, Susan Louise

; APPLICANT: Jiang, Yumi

; APPLICANT: Xu, Jiangchun

; APPLICANT: Mitcham, Jennifer Lynn

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.42708

; CURRENT APPLICATION NUMBER: US/09/352.616A

; CURRENT FILING DATE: 1999-07-13

; NUMBER OF SEQ ID NOS: 472

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 366

; LENGTH: 1851

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-352-616A-366

Query Match 69.2%; Score 546; DB 4; Length 1851;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 237 CGCTTGGGAGACTACGATGACAGCGCTTCATGGATCCCGAGTACCACGTCATGGAGA 296
Db 944 CGCTTGGGAGACTACGATGACAGCGCTTCATGGATCCCGAGTACCACGTCATGGAGA 895
QY 297 AGATCTGCAAGCTCCACAGAGCTGCTGCTGGTGGGTAAAGTCCCAAGAAAGGATCTCAT 356
Db 884 AGATCTGCAAGCTCCACAGAGCTGCTGCTGGTGGGTAAAGTCCCAAGAAAGGATCTCAT 825
QY 357 CGTCATGCTCAGGACACTGATGTGAACAAGAGGCAACAAGAAAGGAGTCTCTACA 416
Db 824 CGTCATGCTCAGGACACTGATGTGAACAAGAGGCAACAAGAAAGGAGTCTCTACA 765
QY 417 TCTGCTCTGCCAATGGAAATCAGAAAGTAGTAAATCTGCTGCTGACACGATGTCA 476
Db 764 TCTGCTCTGCCAATGGAAATCAGAAAGTAGTAAATCTGCTGCTGACACGATGTCA 705

QY 477 ACTTAATGCTCTTGACCAACAAAAAGGAGACGCTCTGACAAAGCGCGTACAATGCCAGA 536
Db 704 ACTTAATGCTCTTGACCAACAAAAAGGAGACGCTCTGACAAAGCGCGTACAATGCCAGA 645
QY 537 AGATGAATGTCGTTAAATGTTGCTGGAACTGGCACTGATCCAAATATTCAGATGAGTA 596
Db 644 AGATGAATGTCGTTAAATGTTGCTGGAACTGGCACTGATCCAAATATTCAGATGAGTA 585
QY 597 TGGAAATACCACTCTACACTATGCTGCTCAATGAAGATAAATTAATGCGCAAGCACT 656
Db 584 TGGAAATACCACTCTACACTATGCTGCTCAATGAAGATAAATTAATGCGCAAGCACT 525
QY 657 GCTCTTATACCGTGTGATATCGAATCAAAAAACAAGCATGGCCCTCACACCACTGCTACT 716
Db 524 GCTCTTATACCGTGTGATATCGAATCAAAAAACAAGCATGGCCCTCACACCACTGCTACT 465
QY 717 TGGTATACATGAGCAAAACAAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCGAATTT 776
Db 464 TGGTATACATGAGCAAAACAAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCGAATTT 405
QY 777 AAATGCGGTGATAGATGGAAGCACTGCTCTCATCTGCTGATGTTGTTGATGATCAGC 836
Db 404 AAATGCGGTGATAGATGGAAGCACTGCTCTCATCTGCTGATGTTGTTGATGATCAGC 345
QY 837 AAGTATAGTACGCTCTACTTGAGCAAAATGTTGATGATCTTCTCAAGATCTGGAAG 896
Db 344 AAGTATAGTACGCTCTACTTGAGCAAAATGTTGATGATCTTCTCAAGATCTGGAAG 285
QY 897 ACGGCCAGAGATGCTGTTTCTAGTCATCATG 933
Db 284 ACGGCCAGAGATGCTGTTTCTAGTCATCATG 248

RESULT 14

US-09-289-198-291/c

; Sequence 291, Application US/09289198

; Patent No. 6586570

; GENERAL INFORMATION:

; APPLICANT: Fridakis, Tony N.

; APPLICANT: Smith, John M.

; APPLICANT: Reed, Steven G.

; APPLICANT: Misher, Lynda

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER

; FILE REFERENCE: 210121.419C5

; CURRENT APPLICATION NUMBER: US/09/289,198

; CURRENT FILING DATE: 1999-04-09

; EARLIER APPLICATION NUMBER: US 09/062,451

; EARLIER FILING DATE: 1998-04-17

; EARLIER APPLICATION NUMBER: US 08/991,789

; EARLIER FILING DATE: 1997-12-11

; EARLIER APPLICATION NUMBER: US 08/838,762

; EARLIER FILING DATE: 1997-04-09

; EARLIER APPLICATION NUMBER: PCT/US97/00485

; EARLIER FILING DATE: 1997-01-10

; EARLIER APPLICATION NUMBER: US 08/700,014

; EARLIER FILING DATE: 1996-08-20

; EARLIER APPLICATION NUMBER: US 08/585,392

; EARLIER FILING DATE: 1996-01-01

; NUMBER OF SEQ ID NOS: 312

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 291

; LENGTH: 1851

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-289-198-291

Query Match 69.2%; Score 646; DB 4; Length 1851;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 237 CGCTTGGGAGACTACGATGACAGCGCTTCATGGATCCCGAGTACCACGTCATGGAGA 296

Db 944 CGCTTGGGAGACTACGATGACAGCGCTTCATGATCCAGGTACACGTCATCGAGA 885
Qy 297 AGATCTGGAGAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAAGAGATCTCAT 356
Db 884 AGATCTGGAGAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAAGAGATCTCAT 825
Qy 357 CGTCATGCTCAGGAGACTGATGTGAACAAGAGGACAAAGAGAGGAGTCTCTTACA 416
Db 824 CGTCATGCTCAGGAGACTGATGTGAACAAGAGGACAAAGAGAGGAGTCTCTTACA 765
Qy 417 TCTGGCTCTGCCAATGGGAATTCAGAGTAGTAAAGTCCGTCGACAGAGATGTCA 476
Db 764 TCTGGCTCTGCCAATGGGAATTCAGAGTAGTAAAGTCCGTCGACAGAGATGTCA 705
Qy 477 ACTTAATGTCTTGAACAACAAAAGAGAGAGTCTGACAAAGGCGGTCAATGCCAGGA 536
Db 704 ACTTAATGTCTTGAACAACAAAAGAGAGAGTCTGACAAAGGCGGTCAATGCCAGGA 645
Qy 537 AGATGAATGTGGTAAATGTTGCTGGAACATGGCACTGATCCAAATATCCAGATGATA 596
Db 644 AGATGAATGTGGTAAATGTTGCTGGAACATGGCACTGATCCAAATATCCAGATGATA 585
Qy 597 TGGAAATACCACTCTACACTATGCTGTCAATGAAGATAAATTAATGGCCAAAGCACT 656
Db 584 TGGAAATACCACTCTACACTATGCTGTCAATGAAGATAAATTAATGGCCAAAGCACT 525
Qy 657 GCTCTTATACGCTGCTGATATGGAAGAGTCTCTCATACTTCTCATCTGATGTTGGATCAGC 836
Db 524 GCTCTTATACGCTGCTGATATGGAAGAGTCTCTCATACTTCTCATCTGATGTTGGATCAGC 345
Qy 837 AAGTATAGTCAGCCCTCTACTTGGAGCAAAATGTTGATGATCTTCTCAAGATCTGGAAG 896
Db 344 AAGTATAGTCAGCCCTCTACTTGGAGCAAAATGTTGATGATCTTCTCAAGATCTGGAAG 285

RESULT 15

US-09-289-198-292/c
; Sequence 292, Application US/09289198
; Patent No. 6586570
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Miser, Lynda
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C5
; CURRENT APPLICATION NUMBER: US/09/289,198
; EARLIER APPLICATION NUMBER: US 09/062,451
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: US 08/991,789
; EARLIER FILING DATE: 1997-12-11
; EARLIER APPLICATION NUMBER: US 08/838,762
; EARLIER FILING DATE: 1997-04-09
; EARLIER APPLICATION NUMBER: PCT/US97/00485
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: US 08/700,014
; EARLIER FILING DATE: 1996-08-20
; EARLIER APPLICATION NUMBER: US 08/585,392
; EARLIER FILING DATE: 1996-01-01

; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 292
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-289-198-292

Query Match 69.2%; Score 646; DB 4; Length 1851;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;

Matches 596; Conservative 0;

Qy 237 GCCTTGGGAGACTACGATGACAGCGCTTCATGATCCAGGTACACGTCATCGAGA 296
Db 944 CGCTTGGGAGACTACGATGACAGCGCTTCATGATCCAGGTACACGTCATCGAGA 885
Qy 297 AGATCTGGAGAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAAGAGATCTCAT 356
Db 884 AGATCTGGAGAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAAGAGATCTCAT 825
Qy 357 CGTCATGCTCAGGAGACTGATGTGAACAAGAGGACAAAGAGAGGAGTCTCTTACA 416
Db 824 CGTCATGCTCAGGAGACTGATGTGAACAAGAGGACAAAGAGAGGAGTCTCTTACA 765
Qy 417 TCTGGCTCTGCCAATGGGAATTCAGAGTAGTAAAGTCCGTCGACAGAGATGTCA 476
Db 764 TCTGGCTCTGCCAATGGGAATTCAGAGTAGTAAAGTCCGTCGACAGAGATGTCA 705
Qy 477 ACTTAATGTCTTGAACAACAAAAGAGAGAGTCTGACAAAGGCGGTCAATGCCAGGA 536
Db 704 ACTTAATGTCTTGAACAACAAAAGAGAGAGTCTGACAAAGGCGGTCAATGCCAGGA 645
Qy 537 AGATGAATGTGGTAAATGTTGCTGGAACATGGCACTGATCCAAATATCCAGATGATA 596
Db 644 AGATGAATGTGGTAAATGTTGCTGGAACATGGCACTGATCCAAATATCCAGATGATA 585
Qy 597 TGGAAATACCACTCTACACTATGCTGTCAATGAAGATAAATTAATGGCCAAAGCACT 656
Db 584 TGGAAATACCACTCTACACTATGCTGTCAATGAAGATAAATTAATGGCCAAAGCACT 525
Qy 657 GCTCTTATACGCTGCTGATATGGAAGAGTCTCTCATACTTCTCATCTGATGTTGGATCAGC 836
Db 524 GCTCTTATACGCTGCTGATATGGAAGAGTCTCTCATACTTCTCATCTGATGTTGGATCAGC 345
Qy 837 AAGTATAGTCAGCCCTCTACTTGGAGCAAAATGTTGATGATCTTCTCAAGATCTGGAAG 896
Db 344 AAGTATAGTCAGCCCTCTACTTGGAGCAAAATGTTGATGATCTTCTCAAGATCTGGAAG 285
Qy 897 ACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933
Db 284 ACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 248

Search completed: April 30, 2004, 16:07:59

Job time : 99 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 14:03:48 ; Search time 2520 Seconds
(without alignments)
11056.117 Million cell updates/sec

Title: US-10-079-137B-343

Perfect score: 933
Sequence: 1 atgggttgaggtaggttc.....tggttcctagtcacatcg 933

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size: 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pin:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rtd:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541	58.0	621	12 BM763942	BM763942 K-EST0045
2	490	52.5	633	12 BM763453	BM763453 K-EST0044
3	177	19.0	865	10 BF676987	BF676987 602084215
4	166	17.8	380	10 BF329652	BF329652 RC6-BN027

C	5	97	10.4	607	28	B48260
	6	94	10.1	729	13	BU910826
	7	89	9.5	400	28	AQ141119 HS_3122A
	8	74	7.9	505	13	EX492731 DFEZp781C
	9	71	7.6	894	10	BF675049 602136643
C	10	58	6.2	279	12	BI461255 603206584
	11	49	5.3	451	9	AI804733 tu42b03.X
	12	47	5.0	531	28	AQ615477 HS_5144_B
	13	43	4.6	544	9	AL703938 DKFZp686E
	14	43	4.6	592	28	AQ372700 RPCI11-6K4
	15	39	4.2	187	10	BE089869 CMI-BR039
	16	35	3.8	694	12	BG720647 602692528
C	17	30	3.2	674	29	AG180921 Pan trogl
	18	29	3.1	477	28	AQ596029 HS_2116_B
	19	29	3.1	710	29	AG165908 Pan trogl
	20	27	2.9	652	29	AG054405 Pan trogl
	21	26	2.8	547	13	EX489137 DKFZp686Q
	22	26	2.8	633	13	EX489112
C	23	25	2.7	386	28	AQ134631 HS_3055_B
C	24	25	2.7	388	28	AQ103336 HS_3071_A
C	25	22	2.4	245	28	BZ881822 CH240_279
C	26	22	2.4	597	29	CE411112 tigr-gss-
C	27	21	2.3	365	13	BY776486 BY776486
C	28	21	2.3	395	13	BY608387 BY608387
	29	21	2.3	522	28	BZ909892 CH240_100
	30	21	2.3	650	14	CA172232 SCSFSB107
	31	21	2.3	967	13	BQ959046 AGENCOURT
	32	21	2.3	1141	10	BF682893 602117687
	33	21	2.3	1201	13	BX364413 BX364413
C	34	20	2.1	152	29	BX895445 Arabidops
C	35	20	2.1	240	28	AZ477017 IM0296114
C	36	20	2.1	336	28	AQ697778 HS_5553_A
	37	20	2.1	488	28	AZ025907 RPCI-23-3
C	38	20	2.1	502	28	AQ596426 HS_5198_A
	39	20	2.1	646	29	CE329241 tigr-gss-
C	40	20	2.1	654	13	CA039828 ssalshc50
C	41	20	2.1	725	29	CE284133 tigr-gss-
	42	20	2.1	833	28	BZ442452 BONPO30TF
	43	20	2.1	853	14	CA757900 OE12A02T
	44	20	2.1	884	29	CG934780 MBEMA79TF
	45	19	2.0	183	14	CD959984 SCZ_215_G

ALIGNMENTS

RESULT 1 BM763942 621 bp mRNA linear EST 04-MAR-2002
LOCUS K-EST0045367 S13KMS5 Homo sapiens cDNA clone S13KMS5-25-All 5',
DEFINITION mRNA sequence.

ACCESSION BM763942
VERSION BM763942.1 GI:19093557

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 621)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daefjeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseung@mail.kribb.re.kr
Plate: 25 row A column: 11
High quality sequence stop: 621.

FEATURES		Location/Qualifiers	
source		1..621	
		/organism="Homo sapiens"	
		/mol_type="mRNA"	
		/db_xref="taxon:9606"	
		/clones="S13KMS5-25-All"	
		/tissue_type="myeloma"	
		/cell_line="KMS-5"	
		/lab_host="Top10F"	
		/clone_lib="S13KMS5"	
		/note="Vector; PCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transfection of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."	
ORIGIN			
	Query Match	58.0%; Score 541; DB 12; Length 621;	
	Best Local Similarity	100.0%; Pred. No. 2.1e-279;	
	Matches	541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	393	CAAGCAAAAGAGGAGTCTCTACATCGGCTCTGCCAATGGGAATTCAGAGTAGTAAA	452
Db	1	CAAGCAAAAGAGGAGTCTCTACATCGGCTCTGCCAATGGGAATTCAGAGTAGTAAA	60
QY	453	ACTCGTCTGGACAGAGTGTCAACTTAATGTCCTTGACACAAAAGAGGACAGCTCT	512
Db	61	ACTCGTCTGGACAGAGTGTCAACTTAATGTCCTTGACACAAAAGAGGACAGCTCT	120
QY	513	GACAAAGCCGTACAATGCCAGGAGATGAATGTGGTTAATGTTCTGGACATGGCAC	572
Db	121	GACAAAGCCGTACAATGCCAGGAGATGAATGTGGTTAATGTTCTGGACATGGCAC	180
QY	573	TGATCCAAATATTCAGATGAGTATGAAATACCACTTACACTATGCTGTCTACAAATGA	632
Db	181	TGATCCAAATATTCAGATGAGTATGAAATACCACTTACACTATGCTGTCTACAAATGA	240
QY	633	AGATAAATTAATGCCCAAGACATGCTCTTATACGGTGTGATATCGAATCAAAAACAA	692
Db	241	AGATAAATTAATGCCCAAGACATGCTCTTATACGGTGTGATATCGAATCAAAAACAA	300
QY	693	GCATGGCTCACACCACTGCTACTTGTATATACATGACCAAAACAGCAAGTGTGAAAT	752
Db	301	GCATGGCTCACACCACTGCTACTTGTATATACATGACCAAAACAGCAAGTGTGAAAT	360
QY	753	TTTAATCAAGAAAAGCGAATTAATGCGCTGGATAGATGGAAGAACTGCTCAT	812
Db	361	TTTAATCAAGAAAAGCGAATTAATGCGCTGGATAGATGGAAGAACTGCTCAT	420
QY	813	ACTGCTGTATGTGGATCAGCAAGTATAGTCAGCCCTTACTTTGACAAAATGTGA	872
Db	421	ACTGCTGTATGTGGATCAGCAAGTATAGTCAGCCCTTACTTTGACAAAATGTGA	480
QY	873	TGATCTTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCAT	932
Db	481	TGATCTTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCAT	540
QY	933	G 933	
Db	541	G 541	

RESULT 2

BM763453

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..633

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="S13KMS5-16-All"

/tissue_type="myeloma"

/cell_line="KMS-5"

/lab_host="Top10F"

/clone_lib="S13KMS5"

/note="Vector; PCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transfection of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match

Best Local Similarity

Matches

540; Conservative

0; Mismatches

1; Indels

0; Gaps

0;

QY

393

CAAGCAAAAGAGGAGTCTCTACATCGGCTCTGCCAATGGGAATTCAGAGTAGTAAA

452

Db

1

CAAGCAAAAGAGGAGTCTCTACATCGGCTCTGCCAATGGGAATTCAGAGTAGTAAA

60

QY

453

ACTCGTCTGGACAGAGTGTCAACTTAATGTCCTTGACACAAAAGAGGACAGCTCT

512

Db

61

ACTCGTCTGGACAGAGTGTCAACTTAATGTCCTTGACACAAAAGAGGACAGCTCT

120

QY

513

GACAAAGCCGTACAATGCCAGGAGATGAATGTGGTTAATGTTCTGGACATGGCAC

572

Db

121

GACAAAGCCGTACAATGCCAGGAGATGAATGTGGTTAATGTTCTGGACATGGCAC

180

QY

573

TGATCCAAATATTCAGATGAGTATGAAATACCACTTACACTATGCTGTCTACAAATGA

632

Db

181

TGATCCAAATATTCAGATGAGTATGAAATACCACTTACACTATGCTGTCTACAAATGA

240

QY

633

AGATAAATTAATGCCCAAGACATGCTCTTATACGGTGTGATATCGAATCAAAAACAA

692

Db

241

AGATAAATTAATGCCCAAGACATGCTCTTATACGGTGTGATATCGAATCAAAAACAA

300

QY

693

GCATGGCTCACACCACTGCTACTTGTATATACATGACCAAAACAGCAAGTGTGAAAT

752

Db

301

GCATGGCTCACACCACTGCTACTTGTATATACATGACCAAAACAGCAAGTGTGAAAT

360

QY

753

TTTAATCAAGAAAAGCGAATTAATGCGCTGGATAGATGGAAGAACTGCTCAT

812

Db

361

TTTAATCAAGAAAAGCGAATTAATGCGCTGGATAGATGGAAGAACTGCTCAT

420

QY

813

ACTGCTGTATGTGGATCAGCAAGTATAGTCAGCCCTTACTTTGACAAAATGTGA

872

Db

421

ACTGCTGTATGTGGATCAGCAAGTATAGTCAGCCCTTACTTTGACAAAATGTGA

480

QY

873

TGATCTTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCAT

932

Db

481

TGATCTTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCAT

540

QY

933

G 933

Db

541

G 541

Db 181 TGATCAAAATATCCAGATGAGTATGGAATACCACTTACACTATGCTGCTACAATGA 240
QY 633 AGATAAATTAATGCGCAAGCACTGCTCTTATACGGTCTGATATCGAATCAAAAAACAA 692
Db 241 AGATAAATTAATGCGCAAGCACTGCTCTTATACGGTCTGATATCGAATCAAAAAACAA 300
QY 693 CGATGGCTCTACACCACTGCTACTTGTGATATGATGAGCAAAACAGCAAGTGGTGAAT 752
Db 301 CGATGGCTCTACACCACTGCTACTTGTGATATGATGAGCAAAACAGCAAGTGGTGAAT 360
QY 753 TTTAATCAAGAAAAAAGCAATTTAAATGCGCTGATAGATATGGAAGCACTGCTCAT 812
Db 361 TTTAATCAAGAAAAAAGCAATTTAAATGCGCTGATAGATATGGAAGCACTGCTCAT 420
QY 813 ACTTCTGTATGTTGTGATCAGCAAGTATGATGAGCCCTTACTTGAAGCAAAATGTTGA 872
Db 421 ACTTCTGTATGTTGTGATCAGCAAGTATGATGAGCCCTTACTTGAAGCAAAATGTTGA 480
QY 873 TGTATCTTCTCAAGATCTGGAAGACGCGCAGAGATGATGTTCTTCTAGTCATCATCAT 932
Db 481 TGTATCTTCTCAAGATCTGGAAGACGCGCAGAGATGATGTTCTTCTAGTCATCATCAT 540
QY 933 G 933
Db 541 G 541

RESULT 3
BF676987
LOCUS 865 bp mRNA linear EST 21-DEC-2000
DEFINITION 60208421F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248746 5',
RNA sequence.

ACCESSION BF676987
VERSION BF676987.1 GI:11950882
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 865)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LCCW1067 row: m column: 03
High quality sequence stop: 642.
Location/Qualifiers

FEATURES

source

1..865
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4248746"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggccgctcgcc); Site 2: SfiI
(ggccattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATCTAGAGCGCGAGCGCCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."

ORIGIN

Query Match 19.0%; Score 177; DB 10; Length 865;
Best Local Similarity 99.6%; Pred. No. 2e-83;
Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 623 TCTACATGAAGATAAATTAATGCGCAAGCACTGCTCTTATACGGTCTGATATCGAAT 682
Db 174 TCTACATGAAGATAAATTAATGCGCAAGCACTGCTCTTATACGGTCTGATATCGAAT 233
QY 683 CAAAAACAAGCATGCGCTCACACCACTGCTACTTGTATATACATGACAAAAACAGCAAG 742
Db 234 CAAAAACAAGCATGCGCTCACACCACTGCTACTTGTGTACATGACAAAAACAGCAAG 293
QY 743 TGTGAAATTTTAAATCAAGAAAAAAGCAATTTAAATCGCTGATATGGAAGAA 802
Db 294 TGTGAAATTTTAAATCAAGAAAAAAGCAATTTAAATCGCTGATATGGAAGAA 353
QY 803 CTCTCTCTCATACTTGTGTATGTTGGATCAGCAAGTATAGTCAGCC 850
Db 354 CTCTCTCTCATACTTGTGTATGTTGGATCAGCAAGTATAGTCAGCC 401

RESULT 4

BF329652/c 380 bp mRNA linear EST 22-NOV-2000
LOCUS RC6-BN0276-165600-011-F12 BN0276 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF329652
ACCESSION BF329652
VERSION BF329652.1 GI:11300400
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS

1 (bases 1 to 380)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?ti=RC6&t2=RC6-BN0276-160600-011-F12&t3=2000-06-16&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 99
High quality sequence stop: 379.
Location/Qualifiers

FEATURES

source

1..380
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0276"
/note="Organ: breast normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under low stringency conditions."

```

ORIGIN
Query Match      17.8%; Score 166; DB 10; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.4e-77;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGAGAGCAAGTGGGCACTTTGGAGACACAAACGACTCTCTGTGAA 158
Db 282 CAGGGGAGCGGAGAGCAAGTGGGCACTTTGGAGACACAAACGACTCTCTGTGAA 223
QY 159 GACGCTTGGGAGCAAGAGTGCAGTGGTGTGCTGCTGCTTCCCTGCTGAGGGGAG 218
Db 222 GACGCTTGGGAGCAAGAGTGCAGTGGTGTGCTGCTGCTTCCCTGCTGAGGGGAG 163
QY 219 CGGCAAGAGCAAGTGGGCGTGTGGGAGACTACGATGACAGCGCC 264
Db 162 CGGCAAGAGCAAGTGGGCGTGTGGGAGACTACGATGACAGCGCC 117

RESULT 5
LOCUS B48260/c
DEFINITION B48260 607 bp DNA linear GSS 08-APR-1999
ACCESSION B48260
VERSION B48260.1 GI:2600497
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 607)
Golden, K., Berry, K., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Venter, J.C., Granger, D., Sub, E., Wible, C., de Jong, P. and
Venter, J.C.
Use of BAC End Sequences for Sequence-Ready Map Building
Unpublished (1997)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: madams@igrr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.
FEATURES
Location/Qualifiers
1..607
/organism="Homo sapiens"
/mol_type="Genomic DNA"
/db_xref="GDB:7502163"
/db_xref="taxon:9606"
/clone="RPCI-11-6K4"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/notes="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC11 Human Male BAC Library"

ORIGIN
Query Match      10.4%; Score 97; DB 28; Length 607;
Best Local Similarity 100.0%; Pred. No. 2.2e-40;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 TCTGCCAATGGGAATTCAGAGTAGTAAACTCGTGGACAGACGATGTCAACTTAAT 483

```

```

Db 182 TCTGCCAATGGGAATTCAGAGTAGTAAACTCGTGGACAGACGATGTCAACTTAAT 123
QY 484 GTCCCTTGACACAAAAGAGGAGGACACTCTGACAAAGG 520
Db 122 GTCCCTTGACACAAAAGAGGAGGACACTCTGACAAAGG 86

RESULT 6
LOCUS BU930826
DEFINITION BU930826 729 bp mRNA linear EST 18-OCT-2002
ACCESSION BU930826
VERSION BU930826.1 GI:24119645
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 729)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2943 row: O column: 04
High quality sequence stop: 555.
FEATURES
Location/Qualifiers
1..729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6668956"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_83"
/notes="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgctcgccg); Site 2: SfiI
(ggcattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCGGCGGCGCGGCGGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."

ORIGIN
Query Match      10.1%; Score 94; DB 13; Length 729;
Best Local Similarity 100.0%; Pred. No. 9.1e-39;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 518 AGGCGGTACAAATGCCAGGAAGATGTCGTTAATGTCGTAACATGCAATGCCACTGATC 577
Db 89 AGGCGGTACAAATGCCAGGAAGATGTCGTTAATGTCGTAACATGCAATGCCACTGATC 148
QY 578 CAAATATTCGAGATGAGTATGGAATACCACTCT 611
Db 149 CAAATATTCGAGATGAGTATGGAATACCACTCT 182

RESULT 7
LOCUS AQ124119
DEFINITION HS_3122_A1_C07_MR CIT Approved Human Genomic Sperm Library D Homo

```



```

sapiens Genomic clone Plate=3122 Col=13 Row=E, genomic survey
sequence.
ACCESSION      AQ124119
VERSION        AQ124119.1  GI:3501285
KEYWORDS       GSS.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1 (bases 1 to 400)
AUTHORS        Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
                Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                Hood,L.
TITLE          Sequence-tagged connectors: A sequence approach to mapping and
                scanning the human genome
JOURNAL        Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE        99390589
PUBMED        10449784
COMMENT        Contact: Mahairas GG, Wallace JC, Hood L
                High Throughput Sequencing Center
                University of Washington
                401 Queen Anne Avenue North, Seattle, WA 98109, USA
                Tel: (206) 616-3618
                Fax: (206) 616-3887
                Email: jwallace@u.washington.edu
                Sequence Tagged Connector
                Plate: 3122 row: E column: 13
                Class: BAC ends
                High quality sequence stop: 400.
FEATURES       source
                location/Qualifiers
                1..400
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
                /clone="Plate=3122 Col=13 Row=E"
                /sex="male"
                /clone_lib="CIT Approved Human Genomic Sperm Library D"
                /note="Organ: sperm; Vector: pBelbac11; BAC Clones in
                E-Coli DH10B"
ORIGIN
Query Match      9.5%; Score 89; DB 28; Length 400;
Best Local Similarity 100.0%; Pred. No. 4.1e-36;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 518 AGCGCGTACATGCCAGGAAGATGTCGGTTAAATGTTCTGCGAATGCGACTGATC 577
Db 237 AGCGCGTACATGCCAGGAAGATGTCGGTTAAATGTTCTGCGAATGCGACTGATC 296

QY 578 CAAATATCCAGATGATGAATACC 606
Db 297 CAAATATCCAGATGATGAATACC 325

RESULT 8
BX492731
LOCUS           DXF2p781C0523_r1 781 (synonym: hlcc4) Homo sapiens cDNA clone
DEFINITION     DXF2p781C0523 5', mRNA sequence.
ACCESSION      BX492731
VERSION        BX492731.1  GI:32004516
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1 (bases 1 to 505)
AUTHORS        Bloecker,H., Boecker,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
                Fobo,G., Han,M. and Wiemann,S.
TITLE          EST (Bloecker,H., Boecker,M., Mewes,H.W., Weil,B., Amid,C., et al.)
JOURNAL        Unpublished (2003)
COMMENT        Contact: MIPS
                MIPS

sapiens Genomic clone Plate=3122 Col=13 Row=E, genomic survey
sequence.
ACCESSION      AQ124119
VERSION        AQ124119.1  GI:3501285
KEYWORDS       GSS.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1 (bases 1 to 400)
AUTHORS        Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
                Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                Hood,L.
TITLE          Sequence-tagged connectors: A sequence approach to mapping and
                scanning the human genome
JOURNAL        Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE        99390589
PUBMED        10449784
COMMENT        Contact: Mahairas GG, Wallace JC, Hood L
                High Throughput Sequencing Center
                University of Washington
                401 Queen Anne Avenue North, Seattle, WA 98109, USA
                Tel: (206) 616-3618
                Fax: (206) 616-3887
                Email: jwallace@u.washington.edu
                Sequence Tagged Connector
                Plate: 3122 row: E column: 13
                Class: BAC ends
                High quality sequence stop: 400.
FEATURES       source
                location/Qualifiers
                1..400
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
                /clone="Plate=3122 Col=13 Row=E"
                /sex="male"
                /clone_lib="CIT Approved Human Genomic Sperm Library D"
                /note="Organ: sperm; Vector: pBelbac11; BAC Clones in
                E-Coli DH10B"
ORIGIN
Query Match      9.5%; Score 89; DB 28; Length 400;
Best Local Similarity 100.0%; Pred. No. 4.1e-36;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 518 AGCGCGTACATGCCAGGAAGATGTCGGTTAAATGTTCTGCGAATGCGACTGATC 577
Db 237 AGCGCGTACATGCCAGGAAGATGTCGGTTAAATGTTCTGCGAATGCGACTGATC 296

QY 578 CAAATATCCAGATGATGAATACC 606
Db 297 CAAATATCCAGATGATGAATACC 325

RESULT 8
BX492731
LOCUS           DXF2p781C0523_r1 781 (synonym: hlcc4) Homo sapiens cDNA clone
DEFINITION     DXF2p781C0523 5', mRNA sequence.
ACCESSION      BX492731
VERSION        BX492731.1  GI:32004516
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1 (bases 1 to 505)
AUTHORS        Bloecker,H., Boecker,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
                Fobo,G., Han,M. and Wiemann,S.
TITLE          EST (Bloecker,H., Boecker,M., Mewes,H.W., Weil,B., Amid,C., et al.)
JOURNAL        Unpublished (2003)
COMMENT        Contact: MIPS
                MIPS

```

```

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZp781C0523) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES       source
                location/Qualifiers
                1..505
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="DKFZp781C0523"
                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_lib="781 (synonym: hlcc4)"
                /notes="Vector: pSport1_sfi; Site_1: SfiIA; Site_2: SfiIB;
                cDNA-collection"
ORIGIN
Query Match      7.9%; Score 74; DB 13; Length 505;
Best Local Similarity 100.0%; Pred. No. 5e-28;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 GAGAAGATCTGGACAAGCTCCACAGAGCTGCTGGTGGGTAAGTCCCGAAGATC 352
Db 165 GAGAAGATCTGGACAAGCTCCACAGAGCTGCTGGTGGGTAAGTCCCGAAGATC 224

QY 353 TCATCGTCATGCTC 366
Db 225 TCATCGTCATGCTC 238

RESULT 9
BF675049
LOCUS           602136643F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273139 5',
DEFINITION     mRNA sequence.
ACCESSION      BF675049
VERSION        BF675049.1  GI:11948944
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1 (bases 1 to 894)
AUTHORS        NIH-MGC http://mgi.nci.nih.gov/
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
                Email: cgabbs@mail.nih.gov
                Tissue procurement: CLONETECH Laboratories, Inc.
                cDNA Library Preparation: CLONETECH Laboratories, Inc.
                cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
                DNA sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LCM1088 row: e column: 12
                High quality sequence start: 6
                High quality sequence stop: 576.
                location/Qualifiers
                1..894
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:4273139"
                /lab_host="DH10B (Tl phage-resistant)"
                /clone_lib="NIH_MGC_83"

```

/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
 Site 1: Sfil (ggcgcctggcc); Site 2: Sfil
 (ggccattatggc); 5' and 3' adaptors were used in cloning
 as follows: 5' adaptor sequence: 5'-CAGCGCCATATGGCC-3'
 and 3' adaptor sequence:
 5'-ATTCTAGAGCCGAGGCGGCCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.4
 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA)."

ORIGIN

Query Match 7.6%; Score 71; DB 10; Length 894;
 Best Local Similarity 100.0%; Pred. No. 2.3e-26;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 623 TCTACATGAGATAAATTAATGACCAAGCAGCTCTTATAGCGTGCTGATCGAAT 682
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 135 TCTACATGAGATAAATTAATGACCAAGCAGCTCTTATAGCGTGCTGATCGAAT 194
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 683 CAAAAACAAG 693
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 195 CAAAAACAAG 205
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 10

BI461255 279 bp mRNA linear EST 21-AUG-2001
 LOCUS 603206584F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5272364 5',
 DEFINITION mRNA sequence.

ACCESSION BI461255
 VERSION BI461255.1 GI:15251911

KEYWORDS EST:

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 279)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L14M11687 Row: 9 Column: 21

High quality sequence stop: 236.

Location/Qualifiers

1. .279

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5272364"

/lab_host="DH10B"

/clone_lib="NIH_MGC_97"

/note="Organ: testis; Vector: pBluescriptR (modified

pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI

(gtcgag); Oligo-dt primed using primer

5'-TTTTTTTTTTTTTNN-3', size-selected for average

insert size 2.2 kb and normalized to ROT 5. This is a

primary library enriched for full-length clones and

constructed using the Cap-trapper method (Carninci, in

preparation). Library constructed by M. Brownstein

(NIH/NHGRI, National Institutes of Health). Note: this is

a NIH_MGC Library."

ORIGIN

Query Match 6.2%; Score 58; DB 12; Length 279;
 Best Local Similarity 100.0%; Pred. No. 1.9e-19;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 ATGCGGCTGCTCTTCTGTGAAGAGCCATTGTCTCAGAGCAAGATGGCAAGT 79
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 63 ATGCGGCTGCTCTTCTGTGAAGAGCCATTGTCTCAGAGCAAGATGGCAAGT 6

RESULT 11

AI804733 451 bp mRNA linear EST 07-MAR-2000
 LOCUS tu42b03.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253677 3',
 DEFINITION mRNA sequence.

ACCESSION AI804733

VERSION AI804733

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 451)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 543 Std Error: 0.00

Seq primer: -40UP from Gibco.

Location/Qualifiers

1. .451

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2253677"

/sex="male"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Pr28"

/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)

with a modified polylinker; Plasmid DNA from the

normalized library NCI CGAP Pr22 was prepared, and ss

circles were made in vitro. Following HAP purification,

this DNA was used as tracer in a subtractive hybridization

reaction. The driver was PCR-amplified cDNAs from a pool

of 5,000 clones made from the same library (clones

985608-986759, 110192-1101959, and 121728-1220615).

Subtraction by Bento Soares and M. Fatima Boraldo."

ORIGIN

Query Match 5.3%; Score 49; DB 9; Length 451;
 Best Local Similarity 100.0%; Pred. No. 1.4e-14;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 802 ACTGCTCTCATCTTGTGTATGTTGTGGATCAGCAAGTATAGTCAGCC 850
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 50 ACTGCTCTCATCTTGTGTATGTTGTGGATCAGCAAGTATAGTCAGCC 98

RESULT 12

AQ615477 531 bp DNA linear CSS 15-JUN-1999
 LOCUS HS_5144_B1_G01_T7A RPCI-11 Human Male BAC Library Homo sapiens
 DEFINITION

genomic clone Plate=720 Col=1 Row=N, genomic survey sequence.

ACCESSION AQ615477
 VERSION AQ615477.1 GI:5076753
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 531)
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 93380589
 PUBMED 10449764

COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
 Plate: 720 row: N column: 1
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 531.

FEATURES
 source
 1..531
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clones="plate=720 Col=1 Row=N"
 /sex="male"
 /clone_lib="RPCI-11 Human Male BAC Library"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"

ORIGIN
 Query Match 5.0%; Score 47; DB 28; Length 531;
 Best Local Similarity 100.0%; Pred. NO. 1.7e-13;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 565 CATGGCACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 611
 |||||
 DB 117 CATGGCACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 163
 |||||

RESULT 13
 LOCUS AL703938
 DEFINITION DKFP686E1728 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
 ACCESSION AL703938
 VERSION DKFP686E1728.5
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 544)
 AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,W., Mewes,H.W., Weil,B. and Wiemann,S.

TITLE EST (Ottenwaelder,B., Obermaier,B., Mewes,H.W., Weil,B. and Wiemann,S.)
 JOURNAL Unpublished (2001)
 COMMENT Contact: MIPS
 MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. No sl sequence available.
 This clone (DKFP686E1728) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
 Location/Qualifiers
 1..544
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFP686E1728"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="686 (synonym: hlcc3)"
 /note="Vector: piriplx2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"

ORIGIN
 Query Match 4.6%; Score 43; DB 9; Length 544;
 Best Local Similarity 100.0%; Pred. No. 2.5e-11;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 623 TCTACAATGAAGATAAATAATATGCGCAAGCACTGCTCTTATA 665
 |||||
 DB 91 TCTACAATGAAGATAAATAATATGCGCAAGCACTGCTCTTATA 133
 |||||

RESULT 14
 LOCUS AQ372700
 DEFINITION RPCI11-14712.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-14712, genomic survey sequence.
 ACCESSION AQ372700
 VERSION AQ372700.1 GI:4343723
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 592)
 AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
 TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other GSSs: RPCI11-14712.TV
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeetigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html
 Seq primer: SP6
 Class: BAC ends

FEATURES
 source
 1..592
 Location/Qualifiers

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7556257"
/db_xref="taxon:9606"
/clone="RPCI-11-14712"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
RPC111 Human Male BAC Library"

ORIGIN

Query Match 4.6%; Score 43; DB 28; Length 592;
Best Local Similarity 100.0%; Pred.No. 2.5e-11;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 623 TCTACATGAGATAAATTAATGCGCCAAAGCACTGCTCTTATA 665
|||||
Db 148 TCTACATGAGATAAATTAATGCGCCAAAGCACTGCTCTTATA 190

RESULT 15
BE069869 187 bp mRNA linear EST 09-JUN-2000
LOCUS CM1-BT0397-201299-073-all BT0397 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION BE069869
VERSION BE069869.1 GI:8414519
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 187)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.P., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.G.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=at2=CM1-BT0397-201
299-073-all&tl=1999-12-20&tl=1)
Seq primer: puc 18 forward
High quality sequence start: 82
High quality sequence stop: 141.
Location/Qualifiers
1. 187
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BT0397"
/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Query Match 4.2%; Score 39; DB 10; Length 187;
Best Local Similarity 100.0%; Pred.No. 3e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 673 GATATCGAATCAAAAAACAAGCATGGCGCTCACACACTG 711
|||||
Db 91 GATATCGAATCAAAAAACAAGCATGGCGCTCACACACTG 129

Search completed: April 30, 2004, 16:06:11
Job time : 2524 secs

FEATURES
source